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GenCore version 5.1.6
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OM protein - protein search, using sw model Run on:

January 20, 2004, 13:54:52 ; Search time 21 Seconds (without alignments) 27.477 Million cell updates/sec

US-09-919-703-1 30 1 SVDVEY 6 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

PIR 76:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\*
1: Dir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
		e C	Length	DB		Description
	30	. 0	128	. 2	877671	streptokinase A (E
7	30	00	157	~	AH3460	arsenate reductase
٣	30	00	279	(1	T09620	tin
4	30	100.0	415	~4	BZSO	streptokinase (EC
Ŋ	30	00	440	~	A22801	streptokinase prec
ø	30	8	440	~	027	a)
7	30	8	<b>4</b> #	N	$\alpha$	æ
00	30	00	1274	N	1072	ike
σ	29	Q	186	(7	T31951	hypothetical prote
7.0	29	9	215	N	C97297	probable phosphata
Ξ.	29	9	1207	~	T16011	hypothetical prote
12	29	Ø	1595	N	T31082	endo-1,4-beta-xyla
13	28	3	311	-	IQBS44	E
14	28	3	629	C)	T27619	hypothetical prote
15	27	0	20	N	A60745	E
16	27	0	180	7	C88465	4.
17	27	0	271	~	690898	probable tail fibe
18	27	0	271	~	***	Ω
19	27	0	368	N	JN0848	- 5
20	27	0	368	~	S46435	porin precursor -
21	27	0	371	~	~	porin fomA precurs
22	27	0	375	N	G85631	hypothetical prote
23	27	0	391	N	S61704	
24	27	0	399	N	E70598	PPE
25	27	0	401		QXBP1L	ical p
26	27	0	407	N	G90907	tail
27	27	0	437	~	9606	e tail
28	27	0	437	~	E90996	a)
53	27	0	437	7	9085	e tail

ole tail folle tail folle tail folle tail folle tail folle tail colle tail colle tail colle ABC transporter	na glucosidase pable tail fib bable membrane idase related bable tail fib sin MYO4 - yea ome polyprotei bretical prot betical prot betical prot	ical to fi to fi ical d hyp d hyp ical ical	otherical prot 11[1] dicitra 12 ptsugas - 12 ptsugas - phoprotein ph nylviologen-re phetical parante nylviologen-re phetical at coxymethybila 14day junction 11day junction 11day junction 13ellar motor s gallar motor s protein myxo	hypothetical prote
D90734 C90769 E85816 A85719 A85741 F85584 H81971 C91026	004624 085693 085693 064887 001899 790945 A85794 H64943	AF0727 T08801 T08801 G86413 G86413 D89900 E90062 B70042 AC0033 T44352 A813336	747536 AH3576 BB3655 BB3655 C59304 T33598 T13598 T13598 T13598 T13598 T13598 T13598 T13598 T1455 T14	A81529
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## ALIGNMENTS

Streptococcus pyogenes (fragment)
Streptococcus streptococcus pyogenes (fragment)
C;Species: Streptococcus pyogenes
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 22-Jun-1999
C;Accession: S77671; S77672
R;Kapur, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser
Mol. Microbiol. 16, 509-519, 1995
A;Title: Molecular population genetic analysis of the streptokinase gene of Streptococc
A;Reference number: S77671; MUID:96037795; PMID:7565111
A;Accession: S77671
A;Accession: S77671
A;Residues: 1-128 «KAP>
A;Cross-references: EMBL:U25853; NID:g818908; PIDN:AAA85729.1; PID:g818909
A;Residues: 1-128 «KAP>
A;Cross-references: Extain ET1/M1
A;Accession: S77672
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C;Species: Streptococcus sp.
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Cybace: Lubespiris y Bequence_revision in-Sep-1959 #ceAt_unamye 24-36p-1559
R/Malke, H.; Roe, B.; Ferretti, J.J.
R/Malke, H.; Roe, B.; Ferretti, J.J.
R/Malke, H.; Roe, B.; Ferretti, J.J.
A/Reference number: A22801; MUD:85232082; PMID:2989113
A/Accession: A22801
A/Access
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C;Species: Streptococcus sp.
C;Species: Streptococcus sp.
C;Dacte: 0.1-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 22-Jun-1999
C;Dacession: S02723
R;Walter, F.; Siegel, M.; Malke, H.
Nucleic Acids Res. 17, 1262, 1989
A;Title: Nucleotide sequence of the streptokinase gene from a group-G Streptococcus.
A;Reference number: S02723; MUID:89160265; PMID:2922269
A;Accession: S02723
A;Andecus A;Accession: S02723
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C;Species: Streptococcus "equisimilis"
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
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100.0%; Score 30; DB 1;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0;
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Local Similarity 100.0%; Score 30; DB
Local Similarity 100.0%; Pred. No. 28;
tes 6; Conservative 0; Mismatches
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C;Superfamily: streptokinase
                                                                                                       208 SVDVEY 213
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         9
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AH3460
arrenate reductase [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AH3460
C;Accession: AH3460
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, i. Mazur, M.; Goltaman, B.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3552; FMID:11756688
A;Accession: AH3460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.157 <kUR>
A;Cross-references: GB:Ab008917; PIDN:AAL52851.1; PID:g17983693; GSPDB:GN00190
A;Berinental source: strain 16M
A;Gene: BME11670
A;Map position: I
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T09620
Probable lectin 2 precursor - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T09620
R;Brill, L.M.; Pieternel, V.R.
submitted to the EMBL Data Library, March 1998
A;Description: Legume seed lectin genes: sequence of Mslec2 from Alfalfa, Alfalfa and SwAccession: T09620
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels
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C;Keywords: calcium; glycoprotein; lectin
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-279/Product: probable lectin 2 #status predicted <MAT>
A,Experimental source: strain E2/M3
A,Note: allele 3
C,Genetics:
A,Gene: ska
C,Superfamily: streptokinase
C,Keywords: hydrolase; plasminogen activator; virulence
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A, Gene: lec2
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A;Cross-references: EMBL:Y16754
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114 SVDVEY 119
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Matches 6; Conserv
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AjStatus: preliminary; translated from GB/EMBL/DDBJ
Amolecule type: DNA
A;Residues: 1-1207 - GPU>
A;Cross-references: EMBL:U000S0; NID:9485108; PID:9485110; PIDN:AAAS0695.1; CESP:F09F7..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A,Reference number: A96900, MUID:21359325, PMID:21359325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: C97297
R;Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                                                                                                            A,Cross-references: EMBL:AF016658; PIDN:AAB66044.1; GSPDB:GN00020; CESP:B0047.4
A,Experimental source: strain Bristol N2; clone B0047
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A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable phosphatase, HAD superfamily [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C'Species: Caenorhabditis elegans
C'Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C'Accession: T16011
R;Pauley, A. submitted to the EMBL Data Library, May 1994
A;Description: The sequence of C. elegans cosmid F09F7.
                                           C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                 R; Pauley, A.; Goela, D.; Ozersky, P. submitted to the EMBL Data Library, July 1997 A; Description: The sequence of C. elegans cosmid B0047. A; Reference number: 221102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
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                         ypothetical protein B0047.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Pred. No. 19;
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1; Mismatches
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83.3%; Pred. No. 2
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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SIDVEY 30
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A,Status: preliminary
A,Molecule type: DNA
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                                                                                                      C; Accession: T31951
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A; Introns: 51/2
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R;Walter, F.; Slegel, M.; Malke, H.
Nucleic Acids Res. 17, 1261, 1989
A;Title: Nucleotide sequence of the streptokinase gene from a Streptococcus pyogenes typ A;Reference number: S02724; MUID:89160264; PMID:2646590
A;Accession: S02724
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C,Species: Dunaliella salina
C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Species: Streptococcus pyogenes
C,Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 22-Jun-1999
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A;Cross-references: EMBL:X13400; NID:g47095; PIDN:CAA31766.1; PID:g47096
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A, Cross-references: EMBL:X13399; NID:947435; PIDN:CAA31765.1; PID:947436
C, Genetics:
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                                                                                                                                                                               100.0%; Score 30; DB 2; Length 440; 100.0%; Pred. No. 28; 0; Indels ive 0; Mismatches 0; Indels
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                                                        A,Gene: skg
C,Superfamlly: streptokinase
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-440/Product: streptokinase #status predicted <MAT>
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C;Superfamily: streptokinase
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-440/Product: streptokinase #status predicted <MAT>
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A;Molecule type: mRNA
A;Residues: 1-1274 <FIS>
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C;Date: 16-Uul-1999 #sequence_revision 16-Uul-1999
C;Accession: 110729
R;Fisher, M.; Gokhman, I.; Pick, U.; Zamir, A.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z17101
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100.0%; Pred. No. 90;
ive 0; Mismatches
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Best Local Similarity 100.
6: Conservative
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                                                                                                                                                                                                                                                                                                                                 183 SVDVEY 188
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Matches 6; Conserv
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Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A, Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekfiguchh, J.; Sekowska, A.; Serol akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Toganoi, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Tanaka, H.; Tanaha, T.; Terpetra, P.; Tosato, V.; Uchiyama, A, Authors: Yoshikawa, H.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A, Title: The complete genome sequence of the Gram-postive bacterium Bacillus subtilis. A, Accession: F69517
A, Accession: F69517
A, Residues: nucleic acid sequence not shown; translation not shown
A, Residues: 1-311 < KUN
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A,Gross-references: GB:Z99118, GB:AL009126; NID:g2635200; PIDN:CAB14858.1; PID:g2635363
A,Experimental source: strain 168
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C;Species: Fusobacterium nucleatum
C;Species: Fusobacterium nucleatum
C;Species: Fusobacterium nucleatum
C;Accession: A60743
R;Bakken, V.; Aaro, S.; Jensen, H.B.
B;Bakken, V.; Aaro, S.; Jensen, H.B.
J; Gen. Microbiol. 135, 3253-3262, 1362, 1371ble: Purification and partial characterization of a major outer-membrane protein A;Reference number: A60745; MUID: 90257576; PMID: 2636259
A;Residues: L50 < Bakk>
A;Residues: 1-50 < Bakk>
A;Note: sequences of the homologous protein from strains F6, F3, and ATCC 10953 were of the homologous protein from strains F6, F3, and ATCC 10953
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A,Introns: 11/3; 63/1; 114/3; 166/2; 187/3; 233/3; 348/2; 405/1; 431/2; 473/1; 581/3
C,Superfamily: acerylcholine receptor
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Cybecies Caenorhabditis elegans
Cybecies 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
CyAccession: T27619
RyKershaw, J

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93.3%; Score 28; DB 2; Length 629;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
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C.Keywords: ATP; nucleotide binding; P-loop
F;168-175/Region: nucleotide-binding motif A (P-loop)
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58;
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nes 4, Conservative
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200 SIDIEY 205
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SIDIEY 98
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Drimosome component (helicase loader) dnaI - Bacillus subtilis

C, Species Bacillus subtilis

C, Species Bacillus subtilis

C, Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 19-Jan-2001

C, Accession: B24720; C25680; F56617

R, Ogasawara, N.; Moriya, S.; Mazza, P.G.; Yoshikawa, H.

Nucleic Acids Res. 14, 9989-9999, 1986

A, Title: Nucleotide sequence and organization of dnaB gene and neighbouring genes on the A, Reference number: A93650; MUD:87117549; PMID:3027671

A, Molecule type: DNA

A, Residues: 1-311 < CGA>

A, Residues: 1-312 < CGA>

A, Residues: 1-314 < CGA>

A, Residues: 1-315 < CGA>

A, Residues: 1-315 < CGA>

A, Residues: 1-315 < CGA>

A, Residues: 1-316 < CGA>

A, Residues: 1-317 < CGA>

A, Residues: 1-317 < CGA>

A, Residues: 1-318 < CGA

A, Residues: 
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C;Species: Caldicellulosiruptor sp.
C;Species: Caldicellulosiruptor sp.
C;Apacesion: T31082
R;Morris, D.D.; Gibbs, M.D.; Ford, M.; Thomas, J.; Bergquist, P.L.
S;Description: Family 10 and 11 xylanase genes from Caldicellulosiruptor sp. Rt69B.1.
A;Reference number: Z20972
A;Accession: T31082
A;Accession: T31082
A;Accession: T31082
A;Accession: T31082
A;Molecule type: DNA
A;Residues: 1-1595 *MOR>
A;Cression: Caldicellulosiruptor sp. Rt69B.1.
A;Coession: T31082
A;Genetics:
A;Geneti
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                                                                                                                                                       A;Gene: CESP:F09F7.3
A;Introns: 23/1; 297/3; 600/2; 630/2; 724/3; 789/3; 916/1; 1102/2; 1150/3
C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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                                            A; Experimental source: strain Bristol N2
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Best Local Similarity 83.3%;
Matches 5; Conservative 1
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accesion: BSD42
R;Perna, N.T.; Plunket III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Accesion: B85642
A;Accesion: B85642
A;Accesion: B85642
A;Accesion: B85642
A;Residues: 1-271 <STO>
A;Residues: 1-271 <STO>
A;Residues: 1-271 <STO>
A;Residues: 1-271 <STO>
A;Reperimental source: strain Ol57:H7, substrain EDL933
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C;Species: Rusobacterium nucleatum
C;Species: Rusobacterium nucleatum
C;Species: Rusobacterium nucleatum
C;Date: 14-Uul-1995 #sequence_revision 21-Uul-1995 #text_change 17-Nov-2000
C;Accession: 846435; 851507
R;Boletad, A.I.; Tommassen, U.; Jensen, H.B.
Mol. Gen. Genet. 244, 104-110, 1994
Mol. Gen. Genet. 244, 104-110, 1994
A;Title: Sequence variability of the 40-kDa outer membrane proteins of Fusobacterium nu A;Reference number: 846435
A;Accession: 846435
A;Status: preliminary
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83.3%; Pred. No. 1.2e+02;
ive 1; Mismatches 0; Indels
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Pred. No. 86;
1; Mismatches
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R;Bolstad, A.I.
Bolstad, C. the EMBL Data Library, August 1994
A;Reference number: S51507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Fusobacterium nucleatum
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conserv
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59 SVDVQY 64
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S46435
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                                                                                                                                                                                                                                                                                                                                                                                                                              protein B0244.9 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C88465
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Rintle: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 1999; Science 283, 2103, 1999; and A;Status: preliminary
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(990898
probable tail fiber protein [imported] - Escherichia coli (strain 0157:H7, substrain RIM c)Species: Escherichia coli
C)Species: Escherichia coli
C)Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C)Accession: G90898
R)Haysshi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, R.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gence A;Reference number: A96629; MUID:21156231; PMID:11258796
A;Accession: G90898
A;Accession: G90898
A;Retuer preliminary
A;Residues: 1-271 cHAX>
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B85842
hypothetical protein Z3309 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:chr_III; PIDN:AAA68377.1; PID:g861357; GSPDB:GN00021; CESP:B0244.
C;Genetics:
A;Gene: B0244.9
A;Map position: 3
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC82159
                                                                                                                                             Gaps
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                                                                             Length 50;
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Pred. No. 86;
1; Mismatches
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د.
                                                                          Score 27; DB 2
Pred. No. 13;
1; Mismatches
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Pred. No. 55;
1; Mismatches
                                                                                90.0%;
83.3%;
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83.3%;
                                                                             Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5, Conservative
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                C; Keywords: membrane protein
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SVDVQY 43
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Best Local Similarity
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A; Residues: 1-180 <S'
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: 17-011-1998 #sequence_revision 17-011-1998 #text_change 22-Oct-1999
C;Accession: E70598
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Accession: E70500; MUID:98295987; PMID:9634230
A;Accession: E70598
A;Accession: E70598
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A; Residues: 1.391 (RIE>
A; Residues: 1.391 (RIE>
A; Residues: 1.391 (RIE>
A; Experimental source: strain S288C (AB972)
A; Cross-references: EMBL: 273586; NID:g1370475; PID:e246942; PID:g1370476; MIPS:YPL230w
A; Crestarazu, L.A.; Vissers, S.
B; Urrestarazu, L.A.; Vissers, S.
B; Urrestarazu, L.A.; Vissers, S.
A; Molecule to the Protein Sequence Database, May 1996
A; Reference number: S65251
A; Rocession: S6525
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Rosidues: 1-91 <URA>
A; Cross-references: EMBL: 273586; NID:g1370475; PID:e246942; PID:g1370476; MIPS:YPL230w
A; Experimental source: strain S288C (AB972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispeciaes: Saccharomyces cerevision 12-Apr-1996 #text_change 19-Apr-2002 Cispeciaes: Saccharomyces cerevision 12-Apr-1996 #text_change 19-Apr-2002 Cispates: 09-Mar-1996 #sequence revision 12-Apr-1996 #text_change 19-Apr-2002 Ciscession: S61704; S65249; S65255 Ribrestaratu, L.A. submitted to the EMBL Data Library, December 1995 A;Reference number: S61699 A;Rocession: S61704 A;Molecule type: DMR A;Residues: 1-391 cura. S6169 A;Residues: 1-391 cura. S6169 A;Residues: BMBL:X94561; NID:g1181252; PID:e217970; PID:g1181258 Righteger, M.; Mueller-Auer, S.; Schaefer, M. Submitted to the Protein Sequence Database, May 1996 A;Reference number: S65202 A;Recession: S65249.
                                                                                                                                                                                                        Gaps
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N.Alternate names: hypothetical protein P1421
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1382
C;Superfamily: phage lambda hypothetical protein 401
                                                                                                                                              90.0%; Score 27; DB 2; 183.3%; Pred. No. 1.2e+02; ive 1; Mismatches 0
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Pred. No. 1.3e+02;
1; Mismatches 0
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Similarity 83.3%;
5; Conservative
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A;Cross-references: SGD:S0006151
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Matches 5, Conserv
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Best Local Similarity
Matches 5; Conserv
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NyAlternate names: major outer membrane protein, 40K
NyAlternate names: major outer membrane protein, 40K
Species: Fusobacterium nucleatum
A;Variety: ATCC 10953 #sequence_revision 21-Jul-1995 #text_change 08-Oct-1999
C;Accession: S46436; S51508
R;Bolstad, A.I.; Tommassen, J.; Jensen, H.B.
Mol. Gen. Genet. 244, 104-110, 1994
A;Tile: Sequence variability of the 40-kDa outer membrane proteins of FusobA;Reference number: S46435; MUID:94316187; PMID:8041356
A;Accession: S46436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: Status: DNA
A,Residues: 1371 &BMB.:X72583
A,Experimental source: ATCC 10953
B,Bolatad, A.I.
B,Bolatad, A.I.
B,Bolatad, A.I.
B,Reference number: S51508
A,Reference number: S51508
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 138, '8',40-338,'G',340-363,'S',365-371 <BOW>
A,Ross-references: EMBL:X72583, NID:g551439, PIDN:CAA51173.1; PID:g551440
A,Experimental source: ATCC 10953
                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156,'K',158-368 <BO2>
A;Cross-references: EMBL:X72582; NID:g530295; PIDN:CAA51172.1; PID:g530296
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                                                                                                                                                                     90.0%; Score 27; DB 2; Length 368
83.3%; Pred. No. 1.2e+02;
ive 1; Mismatches 0; Indels
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83.3%; Pred. No. 1.2e+02;
.ive 1; Mismatches 0; Indels
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-371/Product: porin #status predicted <MAT>
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Matches 5, Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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SVDVQY 64
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probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RI C;Species: Escherichia coli (cjate: 18-Uul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002 C;Accession: E90968 R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Fitle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: E90568 A;Accession: E90568 A;Accession: E90568 A;Accession: E90568 A;Residues: 1-437 cHAV> A;R
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C;Species: Escherichia coli
C;bete: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Jun-2002
C;Accession: H90854
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Cibace: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Jun-2002
Cipacesion: 1990996
Cipacession: 1990996
Cipacession: 199096
Cipacession: 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and cipacession: 19996
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A,Molecule type: DNA
A,Rebidues: 1-437 cHMY>
A,Cross-references: GB:BA000007; PIDN:BAB36364.1; PID:g13362410; GSPDB:GN00154
A,Experimental source: strain O157:H7, substrain RIMD 0509952
C,Genetics:
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83.3%; Pred. No. 1.5e+02;
.ive 1; Mismatches 0; Indels
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C;Superfamily: phage lambda hypothetical protein 401
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C,Superfamily: phage lambda hypothetical protein 401
    Mismatches
1;
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5; Conservative
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SMDVEY 55
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G90907
probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM C.Species: Escherichia coli
C.Species: Escherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C.Accession: G90907
R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Grawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A./Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genchylate ference number: A99629; MUID:21156231; PMID:11258796
A.Accession: G90907
A.Accession: G90907
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-407 < AAX>
A.Cross-references: GB:BA000007; PIDN:BAB35654.1; PID:g13361697; GSPDB:GN00154
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A.Accession: G43010
A.Rededude: 1-401 cDAN>
A.Accession: G43010
A.Residude: 1-401 cDAN>
R.Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.
B.Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.
A.Title: Nucleotide sequence of bacteriophage lambda DNA.
A.Reference number: A92891; MUD:83189071; PMID:6221115
A.Accession: B3016
A.Accessio
    A;Molecule type: DNA
A;Residues: 1-399 <COL>
A;Residues: 1-399 <COL>
A;Cross-references: GB:Z94121; GB:AL123456; NID:g3261736; PIDN:CAB08082.1; PID:e312285;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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QXBP1L

hypothetical protein 401 - phage lambda

hypothetical protein 401 - phage lambda

Sylternate names: orf-401; orf401

C;Species: phage lambda

C;Date: 13-Unn-1983 #sequence_revision 13-Jun-1983 #text_change 23-Jul-1999

C;Accession: G43010; D43016; Ā04389

R;Daniels, D.

submitted to the Nucleic Acid Sequence Database, September 1982
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Pred. No. 1.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      Score 27; DB 2; Length 399
Pred. No. 1.3e+02;
1; Mismatches 0; Indels
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A.Gene: ECs2231
C.Superfamily: phage lambda hypothetical protein 401
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Pred. No. 1.4e+02;
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Best Local Similarity 83.3
Matches 5; Conservative
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| 50 SMDVEY 55
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Best Local Similarity
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C; Superfamily: phage lambda hypothetical protein 401
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C90769
probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C; Accession: C90769
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A; Accession: C90769
A; Title: Complete genome sequence of enterohemorrhagic Scherichia coli O157:H7 and genc A; Reference number: A99629; MUID:21156211; PMID:11258796
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-439 c.HAX>A; Residues: ECSII23
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C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Jun-2002
C.Accession: D90734
R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A.DA, Res. 8, 11-22, 2001
A.JA.ference number: A99629; MulD:21156231; PMID:11258796
A.Scatus: preliminary
A.Scatus: preliminary
A.Residues: 1-438 <HAY.
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A. Z. 2001.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90654
A;Cesserion: H90654
A;Residue: preliminary
A;Residues: 1-437 <AAx>
A;Residues: 1-437 <AAx
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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Pred. No. 1.5e+02;
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C;Superfamily: phage lambda hypothetical protein 401
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Best Local Similarity 83.3°,
"...hes 5; Conservative
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Best Local Similarity 83.34
Est Local Similarity 5, Conservative
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50 SMDVEY 55
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SMDVEY 56
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Probable tail fiber protein of prophage CP-9330 Z2147 [imported] - Escherichia coli (St C; Species: Escherichia coli diate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 03-Jun-2002 C; Accession: A85719

R; Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Gorobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Accession: A85719

A; Status: preliminary
A; Accession: A85719
A; Status: preliminary
A; Accession: A85719
A; Status: DNA
A; Residues: Lype: DNA
A; Residues: Lype: DNA
A; Residues: Lype: DNA
A; Residues: Lype: DNA
A; Cross-references: GB:AE005174; NID:g12515104; PIDN:AAG56213.1; GSPDB:GN00145; UWGP:Z2
A; Cross-references: Strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: Z2147
C; Superfamily: phage lambda hypothetical protein 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable tail fiber protein of prophage CP-933U 23074 [imported] - Escherichia coli (st. Species: Bscherichia coli (5.Species: BsS816 
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     Length 439;
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A,Gene: Z3074
C,Superfamily: phage lambda hypothetical protein 401
90.0%; Score 27; DB 2; I
83.3%; Pred. No. 1.5e+02;
iive 1; Mismatches 0
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Best Local Similarity 83.34
....hes 5; Conservative
     Query Match 90.0
Best Local Similarity 83.3
Matches 5, Conservative
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52 SMDVEY 57
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RESULT 38
E96830
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hypothetical protein Z2340 [imported] - Escherichia coli (strain O157:H7, substrain EDL9 C;Species: Escherichia coli (c;Species: Escherichia coli (d;Species: Esc
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUDD:21074935; PMID:11206551
A;Accession: F85584
A;Status: preliminary
A;Accession: F85584
A;Cross-references: GB:AE005174; NID:g12513753; PIDN:AAG55138.1; GSPDB:GN00145; UWGP:209
A;Cross-references: GB:AE005174; NID:g12513753; PIDN:AAG55138.1; GSPDB:GN00145; UWGP:209
A;Cross-references: Strain O157:H7, substrain EDL933
C;Genetics: A;Gene: 20982
C;Superfamily: phage lambda hypothetical protein 401
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H81971
probable ABC transporter ATP-binding protein NWA0535 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Peb-2001
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Peb-2001
R;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C; Klee, S.R.; Morel; Holroyd, S; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Aritie: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81971
A;Status: preliminary
A;Residues: 1-621 cPAR>
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53 SMDVEY
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ABC transporter, ATP-binding protein NWB1919 [imported] - Neisseria meningitidis (strai c) Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
R;Tettellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
Ti, H.; Olin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Tette: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Reterences: Dreliminary
A;Molecule type: DNA
A;Residues: 1-621 <TET->
A;Cross-references: GB:AE002541; GB:AE002098; NID:97227175; PIDN:AAF42249.1; PID:972271
A;Exmental source: serogroup B, strain MCS8
C;Genetics:
A;Gene: NMB1919
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: B5830
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-831 csTo>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83829.1; PID:g73792
A;Experimental source: serogroup A, strain 22491
CGenetics:
A;Genetics:
A;Genetics:
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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C;Genetics:
A;Gene: F18B13.1
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Pred. No. 2.2e+02;
1; Mismatches 0; Indels
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Local Similarity 83.3%;
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C;Superfamily: heat shock protein
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380 NVDVEY 385
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Best Local S
Matches 5
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peptidase related protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: D90387
R;She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-973 <STO>
A;Cross-references: GB:AE005174; NID:g12514847; PIDN:AAG56007.1; GSPDB:GN00145; UMGP:Z1
A;Experimental source: strain O157:H7, substrain EDL933
A;Gene: Z1918
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C;Species: Escherichia coli
C;Species: L2-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G64887; #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G64887; #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A;Reference 277, 1453-14597
A;Reference 277, 1453-14597
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64887
A;Accession: G64887
A;Accession: G64887
A;Anolecule type: DNA
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A;Residues: 1-1077 <KUR>
A;Cross-references: GB:AE006641; NID:g13015479; PIDN:AAK42355.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO2181
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Pred. No. 4e+02;
1; Mismatches 0; Indels
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90.0%; Score 27; DB 2; I
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0;
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Similarity 83.3%;
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52 SMDVEY 57
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                      Ugabage (EC 3.2.1.20) - Rhizomucor circinelloides f. circinelloides c. Species: UG4624; PC4149

R; Sudimoto, M.; Suzuki, Y.
J. Biochem. 119, 500-505, 1996

A; Title: Molecular cloning, sequencing, and expression of a cDNA encoding alpha-glucosid A; Reference number: UG4624

A; Molecule type: mRNA

A; Residues: 1-84 & SUG1>
A; MOLECULE type: MUD:96271012; PMID:8830045

A; Molecule type: DDBJ:D67034; NID:91498134; PIDN:BAA11053.1; PID:91498135

A; Molecule type: protein
A; Residues: 203-214;492-495;612-623;715-731;742-751;769-778 & SUG2>
A; Molecule type: protein
A; Residues: 203-214;492-495;612-623;715-731;742-751;769-778 & SUG2>
A; Molecule type: protein
A; Residues: 203-214;492-495;612-623;715-731;742-751;769-778 & SUG2>
C; Comment: This enzyme is an exo-carbohydrase, and catalyzes the splitting of an alpha-groundes: alpycoprotein; glycopicaes; hydrolase; sucrase/isomaltase homology; trefoil homolog C; Superfamily: lysosomal alpha-glucosidase; bydrolase
F; 122-805/Domain: sucrase/isomaltase homology <SIM>F; 180,364,406,466,500,568,734/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 19 Probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM C15 probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM C) Species Escherichia coli (Species Escherichia coli C; Date: 18-Uul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C; Accession: B90835 #sequence_revision 18-Jul-2001 R; Hayashi, T.; Maxino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gence A; Accession: B90835 A; Accession: B90835 A; Accession: B90835 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-971 c.HAY A; Robertiannial source: Strain O157:H7, substrain RIMD 0509952 C; Genetics: A; Genetics: Genetics: A; Genetics: Ge
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   Length 831;
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Pred. No. 3.6e+02;
1; Mismatches 0; Indels
                                                                      0; Indels
90.0%; Score 27; DB 2;
83.3%; Pred. No. 3e+02;
iive 1; Mismatches
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Best Local Similarity 83.3
Matches , 5, Conservative
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75 TVDVEY 80
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Volusians 46x protean, 58x protean, 58x protean, 50x protein, cylindrical inclusion polyprocein - papaya ringspot virus

N.Contains 46x protean, 58x protean, 58x
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
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100.0%;
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149 SVDLEY 154
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A; Accession: $30790
A; Cross-references: EMBL: W9057; NID: 917023; PIDN: AAC37409.1; PID: 9172024
A; Cross-references: EMBL: Angust 194
A; Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.
A; Reference number: $5195
A; Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.
A; Reference number: $5195
A; Reference number: $5195
A; Reference number: $5195
A; Reference bind: A; Reference of chromosome 1 of Saccharomyces cerevisiae.
A; Reference number: $5195
A; Reference solved: A; Reference of chromosome 1 of Saccharomyces cerevisiae.
A; Reference number: $5195
A; Reference solved: A; Reference of chromosome 1 of Saccharomyces cerevisiae.
A; Reference number: $5195
A; Reference solved: A; Reference of chromosome 1 of Saccharomyces cerevisiae.
A; Reference number: S5195
A; Reference solved: A; Reference of chromosome 1 of Saccharomyces cerevisiae.
C; Comment: The neck domain comprises six approximately 23-residue tandem repeats; this of Genetics:
A; Gene: SGD: WYO4; SHE1; FUN2; MIPS: YAL029c
A; Gene: SGD: WYO4; SHE1; FUN2; MIPS: YAL029c
A; Map position: IL
C; Superfamily: myosin motor domain homology efforted
C; Reywords actin binding Hateuus predicted
F; 74-765/Domain: myosin motor domain homology efforted
F; 74-765/Domain: coiled coil #status predicted
F; 77-765/Domain: coiled coil #status predicted
F; 1064-147/Domain: carboxyl-terminal #status predicted
F; 1064-147/Binding site: Cys #status predicted
F; 107/Region predicted
A;Residues: 1-1122 <BLAT>
A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74454.1; PID:g1787636; A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74454.1; PID:g1787636; A;Experimental source: strain K-12, substrain MG1655 R;Aiba, H.; Baba, T.; Fujita, K.; Hayashi, K.; Inada, T.; Isono, K.; Itoh, T.; Kasai, H.; Motomura, K.; Nakade, S.; Nakamura, Y.; Nashimoto, H.; Nishio, Y.; Oshima, T.; Saito, Moto, Y.; Horiuchi, T.; Saito, Moto, Y.; Horiuchi, T.; Saito, MA;Res. 3, 363-377, 1996
A;Title: A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the A;Reference number: Z16603; MUID:97251357; PMID:9097039
A;Reference number: Z16603; MUID:97251357; PMID:9097039
A;Accession: T09189
A;Accession: T09189
A;Accession: Dreliminary; translated from GB/EMBL/DDBJ
A;References: CB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74454.1; PID:g1787636;
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NyAlternate names: protein YAL029c
NyAlternate names: protein YAL029c
NyAlternate names: protein YAL029c
CyActes: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002
C;Accession: S30790; S51991
Submitted to the EMBL Data Library, March 1992
A;Description: Identification of a yeast myosin gene that is similar to the
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Pred. No. 5.7e+02;
1; Mismatches 0; Indels
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Pred. No. 4.2e+02;
1; Mismatches 0; Indels
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83.38;
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Local Similarity 83.3%;
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SMDVEY 57
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568 AVDVEY
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Matches 5,
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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero-
B;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AF0727

A;Accession: AF0727

A;Molecule type: DNA

A;Residues: 1-47 <PAR>
A;Residues: 1-47 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05520.1; PID:g16503024; GSPDB:GN00176
C;Generics:
A;Gene: STX1968
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Pred. No. 46;
1; Mismatches
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: H64943
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1455-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64943
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                               A;Cross-references: GB:AE005174; NID:g12515870; PIDN:AAG56813.1; GSPDB:GN00145; UWGP:Z28
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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A,Rebidues: 1-47 - SBLAP
A,Cross-references: GB:A,E000276; GB:U00096; NID:g1788117; PIDN:AAC74894.1; PID:g1788127;
A,Experimental source: strain K-12, substrain MG1655
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AF0727
Conserved hypothetical protein STY1968 [imported] - Salmonella enterica subsp. enterica conserved hypothetical protein STY1968 [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0727
R;Parshill, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M; Dowd, L; White, N.; Farrar, S; Moule, S; O'Gaora, P.
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              5; Conservative
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VDVEY 18
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P50840 escherichia
O93746 aeropyrum p
O81967 thermogue
Q65749 bluetongue
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P5668 bluetongue
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Q65748 bluetongue
Q65748 bluetongue
Q65748 bluetongue
Q65748 bluetongue
P6583 machanococc
Q91214 arabidopsis
P9530 meisseria d
P9530 neisseria m
P6592 neisseria m
P6593 neisseria m
P6599 neisseria m
P6593 neisseria m
P6593 neisseria m
            haematobia
drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Jemalong;
STRAIN=cv. Jemalong;
STRAIN=cv. Jemalong;
MEDLINE=92379255; PubMed=1511126;
Bauchrowitz M.A., Barker D.G., Nadaud I., Rouge P., Lescure B.;
Bauchrowitz M.A., Barker D.G., Nadaud I., Rouge P., Lescure B.;
"Lectin genes from the legume Medicago truncatula.";
Plant Mol. Biol. 19:1011-1017(1992).
-!- MISCELLANBOUS: LECZ IS PROBABLY NON FUNCTIONAL, SINCE A FRAMESHIFT
MUTATION LEADS TO PREMATURE TRANSLATION TERMINATION AFTER ONLY 98
AA. THE SEQUENCE BELOW IGNORES THIS PRAMESHIFT MINATION
-!- MISCELLANBOUS: BINDS ONE MANGANESE (OR OTHER TRANSITION METAL) ION
AND ONE CALCIUM ION. THE METAL IONS ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago truncatula (Barrel medic).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosida I; Rabales; Fabaceae; Papillonoideae; Trifolieae; Medicago.
NCBI_TaxID=3880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Truncated lectin 2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
UVRC MYCBV
ACE HABIE
ACE HABIE
RAPI SCHPO
YERA BACSU
RPC2 MOUSE
YLIE ECOLI
DYP3 BTV11
VP3 BTV2
VP3 BTV3
VP3 BT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMZ ORYSA
GPMI MYCPU
HMZ2 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSV11
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 LEC2_MEDTR
ID _LEC2_MEDTR
 Q01807 medicago tr
P10520 streptococc
P10520 streptococc
P10519 streptococc
Q9cwis wiggleswort
Q9cwis wiggleswort
Q9cwis wiggleswort
Q9cwis wiggleswort
Q9cwis misculu
Q9023 mas misculu
Q9cyb rattus norv
P76072 escherichia
P76072 escherichia
P76072 escherichia
P76072 escherichia
P76072 escherichia
P76072 mucor javan
P76074 homor javan
P76072 escherichia
P7205 escherichia
P7212 escherichia
P7212 escherichia
P7225 escherichia
P7225 escherichia
P7225 escherichia
P7225 escherichia
P7237 mucor javan
P7241 avenory
Q9491 aeropyrum p
Q9491 aerococcus
Q9491 aerococcus
Q9491 mycobacteri
Q9493 mycobacteri
Q9493 thermococcus
Q9493 thermococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                       ; Search time 11 Seconds (without alignments) 25.651 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEC2 MEDTR STREP S
                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries
                                                                             protein search, using sw model
                                                                                                         2004, 13:54:52
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Query
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30
1 SVDVEY 6
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Perfect score:
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Maximum I
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195 1
207 2
298 3
438 4
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                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus
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VARIANT
CONFLICT
CONFLICT
SEQUENCE
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P10520;
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                                                                                                                                                                                                                                                                                                       .
0
                                                                                                    serine proteases.";
Biochmeistry 21:650-6625(1982).
-!- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES
PLASMINOGEN BY COMPLEXING WITH IT. AS POTENTIAL VIRULENCE FACTOR.
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jackson K.W., Tang J.; "Complete amino acid sequence of streptokinase and its homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malke H., Roe B., Ferretti J.J.;
"Nucleotide sequence of the streptokinase gene from Streptococcus
equisimilis H46A.";
Gene 34:357-362[1985].
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                   100.0%; Score 30; DB 1; Length 280; 100.0%; Pred. No. 8.3; o. Mismatches 0; Indels
SACCHARIDE-BINDING AND CELL-AGGLUTINATING ACTIVITIES. SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus equisimilis.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                     DB68690AD8015E81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                440 AA
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MEDLINE=85232082; PubMed=2989113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 27-440.
MEDLINE=83127125; PubMed=6760891;
                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-APR-1988 (Rel. 07, Last seq
15-SBP-2003 (Rel. 42, Last and
Streptokinase C precursor.
                                                                                                                                                                                                                                                            272 N
30473 MW;
                                                                                        EMBL; X60387; CAA42938.1; -. HSSP; P04122; 1LOE.
                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                  148
152
155
1758
1758
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280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus.
NCBI_TaxID=119602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      1 SVDVEY 6
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                                                                                                                                                                                                                                                                                     Query Match
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STRP_STREQ
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AC P00779;
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IT IS THOUGHT TO PREVENT THE FORMATION OF EFFECTIVE FIBRIN BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE INVASIVENESS OF THE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SF170 / AICC 700294 / Serotype M1;
MEDLINE-21192684; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian X., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl., Acad. Sci. U.S.A. 98:4658-4663(2001).
-!- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES
PLASMINGERS BY COMPLEXING WITH IT. AS POTEWTIAL VIRULENCE FACTOR,
IT IS THOUGHT TO PREVENT THE PORMATION OF BFFECTIVE FIBRIN
BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE
INVASIVENESS OF THE CELLS.
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STRAIN=SF130/13 / Serotype M1;
MEDLINE=89160264; PubMed=2646590;
MBLINE=89160264; PubMed=2646590;
MBLOT F., Slegel M., Malke H.;
"Nucleotide sequence of the streptokinase gene from a Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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D -> L.
EXY -> LEYK (IN REF. 2).
N -> D (IN REF. 2).
W -> G (IN REF. 2).
W; 8FC1F22648ACC77A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; K02986; AAA26974.1; -.
EMBL; X72832; CAA51351.1; -.
PIR; A22801; A22801.
PDB; 10QR; 03-MAY-00.
InterPro; IPR04093; Staphylokinase.
Ffam; PF0221; Staphylokinase, 3.
Plasminogen activation; Signal; Virulence; 3D-structure.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Streptokinase A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyogenes type 1 strain.";
Nucleic Acids Res. 17:1261-1261(1989).
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Gaps

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0; Indels

Length 440;

7;

100.0%; Score 30; DB 100.0%; Pred. No. 13;

0; Mismatches

STREPTOKINASE G. 5521F8825FE1B6EA CRC64;

50199 MW;

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440 AA;
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Best Local Similarity
Matches 6; Conserv
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 CHAIN
SEQUENCE
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P81307;
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Y34A METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptcoccus.";

Nucleic Acids Res. 17:1262-1262(1989).

-!- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES

-!- FUNCTION: THIS PROTEIN IS NOT A PROTEINIL VIRULENCE FACTOR,

IT IS THOUGHT TO PREVENT THE FORMATION OF EFFECTIVE FIBRIN

BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE

INVASIVENESS OF THE CELLS.
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                 ..
                                                                                                     EMBL; X13399; CAA31765.1; -.
EMBL; AE006620; AAK34665.1; -.
PIR; S02724, S02724.
FIRPPRO, IPRO04093; Staphylokinase.
Pfam; PF02821; Staphylokinase, 3.
Plasminogen activation; Signal; Virulence; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=89160265; PubMed=2922269;
Walter F., Siegel M., Malke H.;
"Nucleotide sequence of the streptokinase gene from a group-G
                                                                                                                                                                                                                                                                                        100.0%; Score 30; DB 1; Length 440; 100.0%; Pred. No. 13; 13; o; Mismatches 0; Indels
                                                                                                                                                                                                     L -> V (IN REF. 1).
R -> G (IN REF. 1).
D -> N (IN REF. 1).
D -> X (IN REF. 1).
K -> N (IN REF. 1).
K -> N (IN REF. 1).
W, D6227EF040B758DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus sp. (strain 19909).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           440 AA
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Best Local Similarity 100...
6; Conservative
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163
345
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428
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163
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440 AA;
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AC P10519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM Z661 / ATCC 43067;

STRAIN=JAL-1 / DSM Z661 / ATCC 43067;

MEDLINE=96337999; PubMed=86808087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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ID DCUP WIGHER

C 08CWI5.

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annocation update)

OT 15-SEP-2003 (Rel. 42, Last annocation update)

Migglesworthia glossinidia brevipalpis.
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Pred. No. 9.1;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome. SEQUENCE 183 AA; 21756 MW; 769FCF680E86C895 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0347.1.
                                                                                                                                                                                                   183 AA
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.38;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus jannaschii.
                                                                                                                                                                                                   STANDARD;
183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||:||
|1 SVDIEY 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; MJ0347.1;
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REVISIONS
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                                                                                                                                                                             "Genome sequence of the endocellular obligate symbiont of tsetse files, Migglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
-i. CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Andmatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxndale D., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: CYtoplasmic (Probable).
SIMILARITY: BELONGS TO THE UROPORPHYRINGGEN DECARBOXYLASE FAMILY.
                                                                                       SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF 00218; -; 1.
InterPro; IPR006361; HemE.
InterPro; IPR006361; HemE.
InterPro; IPR001257; Uro_decarbxyls.
Prodom; PF01208; URO-D; 1.
Prodom; PF001225; Uro decarbxyls; 1.
TIGRPAMS; TIGR01464; hemE; 1.
PROSITE; P800906; UROD_1; FALSE_NEG.
PROSITE; P8009067; UROD_2; 1.
Lyase; Decarboxylase; Porphyrin biosynthesis; Complete proteome.
SEQUENCE 360 AA; 41359 WW; CA18CB13C1B8492B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.7%; Score 29; DB 1; Length 360; 83.3%; Pred. No. 19; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9VAD6; Q8S2V9; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 15-SBP-2003 (Rel. 42, Last annotation update) Putative conserved oligomeric Golgi complex component 7.
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                                                                                                                                                                                                                                                                                              PATHWAY: Porphyrin biosynthesis.
                          Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB063522; BAC24654.1; -.
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                                             NCBI_TaxID=36870;
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Buckeys D. Rectan M. Bucker H. Sacketein P. Bectler P. Charles C. Besam D. R. Bucker H. Sacketein P. Bectler R. Charles S. Daniele C. Uswenport Lib. Davies D. Potes S. M. Charles S. Daniele C. Danie
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Query Match
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A Azevedo V., Berrero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brotiles R., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Eriz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,
Kurita K., Lapidus A., Ladinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lapidus A., Galleron N., Sorokin A., Ehrlich S.D., "Sequencing and functional annotation of the Bacillus subtilis genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=87117549; PubMed=3027671;
Ogasawara N., Moritya S., Mazza P.G., Yoshikawa H.;
Nucleotide sequence and organization of dnaB gene and neighbouring genes on the Bacillus subtilis chromosome.";
Nucleic Acids Res. 14:9989-9999(1986).
                     Hypothetical protein; Transport; Protein transport; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Bacillus
                                                                                                                                                            ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE=97124191; PubMed=8969504; Mipat A. Carter N., Priper K., Mipat A., Carter N., Brignell C.S., Guy J.B., Piper K., Sanders J., Emmerson P.T., Harwood C.R.; The dnaB-pheA (256 degrees-240 degrees) region of the Bacil subtilis chromosome containing genes responsible for stress metabolism.";
                                                                                                                 Length 742;
                                                                                                                                                            Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                  742 AA; 84075 MW; 85998EF365194E39 CRC64;
                                                                                                                                                            .;
0
                                                                                                             Query Match 96.7%; Score 29; DB 1; Best Local Similarity 83.3%; Pred. No. 41; Matches 5; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN'1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Primosomal protein dnal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the 200 kb rrnB-dnaB region."; Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168;
MEDLINE=98048467; PubMed=9387221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microbiology 142:3067-3078(1996).
PRINTS; PR00747; GLYHDRLASE47.
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                    682 SVDIEY 687
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SEQUENCE FROM N.A.
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P06567;
                                          Membrane.
SEQUENCE
  SKKB
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RA PETEO V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Schyuch J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Scrokin M., Tacconi E., Tanaka T., Tarahashi H., Takemaru K.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Winters P., Wabbut R., Wander E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RY Soshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
R. The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87118226; PubMed=3027697;
Hoshino T., McKenzie T., Schmidt S., Tanaka T., Sueoka N.;
"Nucleotide sequence of Bacillus subtilis dnaB: a gene essential for DNA replication initiation and membrane attachment.";
Proc. Natl. Acad. Sci. U.S.A. 84:653-657(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Archaebacterial virus SSV1 encodes a putative DnaA-like protein.";
Nucleic Acids Res. 20:1143-1143(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95291463; PubMed=7773414;
Bruand C., Ehrlich S.D.;
"The Bacillus subtilis dnal gene is part of the dnaB operon.";
Microbiology 141:1199-1200(1995).
-!- FUNCTION: PROBABLY INVOLVED IN DNA REPLICATION.
-! SIMILARITY: SOME, TO DNAA FROM VARIOUS BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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66.7%; Pred. No. 28;
iive 2; Mismatches 0; Indels
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K -> N (IN REF. 5).

M -> T (IN REF. 5).

7 A86FC94AB6841264 CRC64;
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EMBL; Z99118; CAB14858.1; -...
EMBL; M15183; AAA22405.1; -...
EMBL; B24720; IQBS44.
Subtilist; B010359; dnal.
InterPro; IPR003593; AAA_ATPase.
SMART; SM00382; AAA; 1...
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24 24 M
311 AA; 36114 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-206 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
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tes 4; Conserv
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93 SIDIEY 98
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BY SIMILARITY.

REMOVED IN MATURE FORM (BY SIMILARITY)
TRIPEPTIDYL-PEPTIDASE I.

BY SIMILARITY.

Serine protease; Zymogen; Signal; Lysosome;

EMBL, AJ011912; CAA09863.1; ALT\_INIT. EMBL, AF124599; AAD032573.1; --EMBL, AF111172; AAD03083.1; --EMBL, AK002418; BAB22085.1; --MEROPS; SS3.003; --

MEROPS; S53.003; -. MGD; MGI:1336194; Cln2. Hydrolase; Protease; Se

Glycoprotein. SIGNAL PROPEP 2

CHAIN

ACT\_SITE ACT\_SITE ACT\_SITE CARBOHYD CARBOHYD

NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
N.LINKED (GLCNAC. .) (POTENTIAL).

OAF8163EA1A66396 CRC64; M -> V (IN REF. 1). P -> LDPFVP (IN REF.

CONFLICT CARBOHYD CARBOHYD

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEDLINE-278B/60; PubMed=11217851;

XETAINE-578B/60; Y. Modolorit T. Mondo S., Yamanaka I., Ashburner M., Bandlow S., Casavant T., Ashburner M., Batalow S., Casavant T., Ashburner M., Radlow S., Casavant T., Ashburner M., Radlow S., Casavant T., Ashburner M., Radlow S., Cochima H., Nokido T., Rabloli F., Sizuki R., Tomita M., Radlow M., Barsh G., Barsh G., Borfelli D., Boffelli D., Bolinga N., Carninci P., de Bonaldo M.F., Ashbursein M.J., Bult C., Pletcher C., Pujita M., Gariboldi M., Barsh G., Barsh G., Marchionni L., Mashima J., Mazchionni L., Mashima J., Mazchionni L., Mashima J., Mordone P., Ringy B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Warnkiaw H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Warnkiaw Y., Kawaji H., Kohtsuki S., Warning M., Marning L., Marning L., Marning M., Marning M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1. FUNCTION: Lysosomal Serine protease with tripeptidyl-peptidase I activity. May act as a non-specific lysosomal peptidase which activity. May act as a non-specific lysosomal peptidase which generates tripeptides from the breakdown products produced by lysosomal proteinases. Requires substrates with an unsubstituted N-terminus (By similarity)
-1. CATALYTIY: Release of an N-terminal tripeptide from a polypeptide, but also endopeptidase activity.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99142696; PubMed=9989590;
Vines D.J., Warburton M.J.;
"Classical late infantile neuronal ceroid lipofuscinosis fibroblasts are deficient in lysoscomal tripeptidyl peptidase I.";
FEBS Lett. 443:131-135(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sleat D.E., Lobel P., where the lysosomal pepstatin insensitive protease which is deficient in human classical late infantile neuronal ceroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20028316; PubMed=10556422;
Katz M.L., Liu P.-C., Grob-Nunn S.E., Shibuya H., Johnson G.S.;
"Characterization and chromosomal mapping of a mouse ortholog of the
late-infantile ceroid-lipofuscinosis gene CLN2.";
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Tripeptidyl-peptidase I precureor (EC 34.14.9) (TPP-I) (Tripeptidyl
aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC).
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: Activated by autocatalytic proteolytical processing upon acidification (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO PEPTIDASE FAMILY S53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mamm. Genome 10:1050-1053(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
                                                                                                                               (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipofuscinosis."
                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIU P.-C., Katz M.L., Siakotos A.N., Grob S.E., Johnson G.S.;
Liu P.-C., Katz M.L., Siakotos A.N., Grob S.E., Johnson G.S.;
"Coding sequence and exon/intron organization of the canine CLN2 gene
and its exclusion as the locus for ceroid lipofuscinosis in English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I activity. May act as a non-specific lysosomal peptidase which generates tripeptides from the breakdown products produced by lysosomal proteinases. Requires substrates with an unsubstituted N-terminus (By similarity).

-!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from a
                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Trippeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I) (Tripeptidyl annotectidase) (Lysosomal pepstatin insensitive protease) (LPIC).
CLN2 OR TPP1.
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canie familiarie (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: Activated by autocatalytic proteclytical processing upon acidification (By similarity).
                                                                                                                 ;
                                                                     Score 27; DB 1; Length 562;
Pred. No. 91;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    PRT; 563 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Lygosomal.
                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
                                 61342 MW;
                                                                       Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                    STANDARD;
1
562
562 AA;
                                                                                                                                                                                                 273 SLDVEY 278
                                                                                                                                                           1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide.
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Q9XSB8;
                                 SEQUENCE
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BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-A (IN REF. 2).

VG -> SQ (IN REF. 2).

GGT -> SPP (IN REF. 2).
                                                                EMBL; AB043870; BAB18570.1; -.
Hydrolase; Protease; Serine protease; Zymogen; Signal; Lysosome; Glycoprotein.
SIGNAL 1 19 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 1; Length 563; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                     ; -> SQ (IN REF. 2).

HT -> SPP (IN REF. 2).

B54F3C86205DFEC1 CRC64;
                                                                                                                           BY SIMILARITY.
REMOVED IN MATURE FORM.
TRIPEPTIDYL-PEPTIDASE I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
modified and this statement is not remove
entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 174:1462-1477 (1992)
                                                                                                                                                                                                                                                                                                                                                                                           61332 MW;
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Lambda-like viruses.
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274 SLDVEY 279
                                                                                                                                                                                                                                                                                                                                                                          389
563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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216
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                                                                                                      REMOVED IN MATURE FORM (BY SIMILARITY).

TRIPEPTIDYL-PEPTIDASE 1.

BY SIMILARITY.

NUCLEOPHILE (BY SIMILARITY).

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from rat spleen.",
Biochim. Bi
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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28-FEB-2003 (Rel. 41, Last annotation update)
Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC).
CLN2 OR TPP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Du P., Kato S., Li Y., Maeda T., Yamane T., Yamamoto S., Fujiwara M. Yamamoto Y., Nishi K., Ohkubo I., "Rat tripeptidyl peptidase I: its purification and molecular cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-58323562, PubMed-9659384;
Vines D.J., Warburton M.J.;
"Purification and characterisation of a tripeptidyl aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide.
SUBCELLULAR LOCATION: Lysosomal.
PTM: Activated by autocatalytic proteolytical processing upon
acidification (By similarity).
                                    MEROPS; S53.003; -.
Hydrolase; Protease; Serine protease; Zymogen; Signal; Lysosome;
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 196-217; 374-392 AND 395-429, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                  Score 27; DB 1; Length 563; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                               21465A44C34934F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY S53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          563 AA
                                                                                                                                                                                                                                                                                                                                                       Pred. No. 91;
1; Mismatches
                    EMBL; AF114167; AAD25043.1; -.
                                                                                                                                                                                                                                                                                               61362 MW;
                                                                                                                                                                                                                                                                                                                                  90.0%;
                                                                                                                                                                                                                                                                                                                                                       Similarity 83.3
5; Conservative
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195
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222
286
313
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563 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                            1 SVDVEY 6
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SIGNAL
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CHAIN
ACT SITE
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CARBOHYD
CARBOHYD
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SEQUENCE
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Q9EQV6;
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Gaps

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Indels

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MISCELLANDOUS: The common laboratory strain of bacteriophage lambda, lambda PaPa; carries a frameshift mutation relative to Urlambda, the original isolate. The Urlambda virions have thin, jointed tail fibers (side tail fibers) that are absent from lambda wild type. Relative to lambda PaPa, Urlambda has expanded receptor specificity and adsorbs to E.coli cells more rapidly. SIMILARITY: BELONGS TO THE TAIL FIBER PAMILY.
CAUTION: THIS IS A CONCEPTUAL TRANSLATION, A FRAMESHIFT WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92165720; PubMed=1531648; Haggard-Liungquist E., Halling C., Calendar R.; Hungquist E., Halling C., Calendar R.; Managard-Liungquist E., evidence of the tail fiber genes of bacteriophage P2: evidence for horizontal transfer of tail fiber genes among unrelated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93068310; PubMed=1439823;
Hendrix R.W., Duda R.L.;
"Bacteriophage lambda PPPa: not the mother of all lambda phages.";
Science 258:1145-1148(1992).
dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                        Petersen G.B.;
                                                                                                                                                                                                                                                   MEDLINE=83189071; PubMed=6221115; Sanger F., Coulson A.R., Hong G.F., Hill D.F., Pete Sanger F., Coulson A.R., Hong G.F., Hill D.F., Pete "Nucleotide sequence of bacteriophage lambda DNA."; J. Mol. Biol. 162:729-773 (1982)
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CARBOHYD
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SEQUENCE
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
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or send an email.

NR EMBL; D67034; BAA11053.1; -...

DR InterPro; IPR00322; Glyco_hydro_31.

DR PROSITE; P800129; GLYCOSYL_HYDROL_F31_2; FALSE_NEG.

FROSITE; P800707; GLYCOSYL_HYDROL_F31_2; FALSE_NEG.

TW Hydrolase; Glycoprocein; Signal.

TW Hydrolase; Glycoprocein; Signal.
  CORRECTED IN POSITION TO 396 TO RECREATE THE ORIGINAL STF PRIOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugimoto M., Suzuki Y., "Molecular Clound, sequencing, and expression of a cDNA encoding molecular cloning, sequencing, and expression of a cDNA encoding alpha-glucosidase from Mucor javanicus.";
J. Blochem. 119:500-505(1996).
-I- FUNCTION: Hydrolyzes not only malto-oligosaccharides but also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soluble starch.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      774 AA; 77527 MW; CDD1DF85E919123B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%; Score 27; DB 1; L
83.3%; Pred. No. 1.3e+02;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                             EMBL; J02459; AAA96555.1; ALT FRAME.
EMBL; J02459; AAA96557.1; ALT_FRAME.
PIR; C43009; QXBP2L.
InterPro; IPRO05003; Phage_fiber.
InterPro; IPR005068; Phage_fiber_2.
Pfam; PF03335; Phage_fiber; 6.
Pfam; PF03466; Phage_fiber; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96271012; PubMed=8830045;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.35,
S. Conservative
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50 SMDVEY 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mucor javanicus.
                                                                                                                                                                                                                                                                                                                                                                                                   Fiber protein.
SEQUENCE 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
AGLU MUCJA
AC 092442;
DT 01-NOV-1997
DT 01-NOV-1997
DT 01-NOV-1997
DT 15-SEP-2003
DE Alpha-glucos;
NC EUKATYOLA;
CC EUKATYOLA;
CC EUKATYOLA;
CC EUKATYOLA;
CC MUCCT;
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Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
Takepoto K., Takeuchi Y., Mada C., Manamoto Y., Horiuchi T.,
D., Kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / MG1655,
BIBLINR=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
N-LINKED (GLCNAC. .) (POTENTIAL).
M; CFAB4759DC431403 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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EMBL; D90775; BAA14976.1; ...
ENGL; D90775; BAA14975.1; ...
ECGGENE, EG13370; BLER.
InterPro; IPR005003; Phage_fiber.
InterPro; IPR005068; Phage_fiber_2.
Pfam; PF033406; Phage_fiber_2; 1.
Hypothetical protein; Fiber protein; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                         .
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STRANDARD; PRT; 1120 AA.

AC P76072; P77560;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Side tail fiber protein homolog from lambdoid prophage Rac.
GN STFR OR B1372.
                                                                                                                                                                                                                                                  Score 27; DB 1; Length 864;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000234; AAC74454.1; ALT_INIT.
      364 N-
406 N-
466 N-
560 N-
568 N-
734 N-
98761 MW;
                                                                                                                                                                                                                                                      90.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                         5; Conservative
                               500
500
500
500
568
734
734
77
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     :|||||
75 TVDVEY 80
                                                                                                                                                                                                                                                                                                                                                                               1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=S228C / AB972;
MEDLINE=95249563; PubMed=7731988;
Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
Storms R.K.;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=94334370; PubMed=8056830;
Marer B.K., Petzold A., Lillie S.H., Brown S.S.;
"Identification of MY4, a second class V myosin gene in yeast.";
J. Cell Sci. 107:1055-1064(1994).
                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                      ;
0
                 Score 27; DB 1; Length 1120;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            "The nucleotide sequence of chromosome I from Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M90057; AAC37409.1; -.

BMBL; U12980; AAC05003.1; -.

BIR; S30090; S30790.

HSSP; P10587; 1BR2.

SGD; S0000027; MYC4.

GO; GO:0001043; C:actin cap (sensu Saccharomyces); IDA.

InterPro; IPR0002710; DIL.

InterPro; IPR00048; IQ_region.

InterPro; IPR001609; Myosin_head.

InterPro; IPR01609; Myosin_N.
113779 MW; 542E59D71EE795B4 CRC64;
                                                                                                                                                   (Rel. 27, Created)
(Rel. 27, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                1471 AA
                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00063; myosin head; 1.
Pfam; PF02736; Myosin N; 1.
PRINTS; PR0193; MYOSINHEAVY.
ProDom; PD000355; myosin head; 1.
SMART; SM00015; IQ; 2.
SMART; SM00242; MYSc; 1.
                                                                                                                                                                                Myosin-4 isoform.
MYO4 OR SHE1 OR YAL029C OR FUN22.
                  90.0%;
                                        5; Conservative
                                                                                                                               STANDARD:
1120 AA;
                                                                      |:||||
50 SMDVEY 55
                             Local Similarity
                                                          1 SVDVEY 6
                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                    01-OCT-1993
                                                                                                                               MYS4 YEAST
P32492;
                                                                                                                                                              01-OCT-1993
                                                                                                                                                                        15-SEP-2003
SEQUENCE
                    Query Match
                                        Matches
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MEDLINE=9309098; PubMed=1456896;

MEDLINE=9309098; PubMed=1456896;

MEDLINE=9309098; PubMed=1456896;

MEDLINE=9309098; PubMed=1456896;

MANG C.H., Yeh S.D.;

MILG, and non-papaya infecting strains of papaya ringspot virus.";

LACh. Virol. 127:345-346 (1992).

LACH. Virol. 127:345-346 (1992).

LI Arch. Virol. 127:345-346 (1992).

C. I- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY.

MAY BE INVOLVED IN REPLICATION.

C. I- FUNCTION: VUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

C. I- FUNCTION: WUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

C. I- CATALYIC ACTIVITY: Hydrolyzes Glutaminyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1'

C. Lhat vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLG PRBOWH STANDARD, PRT, 3344 AA.

Q01901;

Q1-0CT-1993 (Rel. 27, Created)

O1-0CT-1996 (Rel. 34, Last sequence update)

28-FBB-2003 (Rel. 41, Last annotation update)

Cenome polyprotein [Contains: N-terminal protein (Pl); Helper component proteinse (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa protein 1 (6K1); Cytoplasmic inclusion protein (Cl); 6 kDa protein 2 (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A) (INIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion protein A (NI-A) (EC 2.7.7.48); Cost protein (CP).

[EC 2.7.7.48); Cost protein (CP).

Papaya ringspot virus (strain P / mutant HA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang C.H., Bau H.J., Yeh S.D.; "Comparison of the nuclear inclusion b protein and coat protein genes of five papaya ringspot virus strains distinct in geographic origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93019006; PubMed=1402799; Yeb. S.D. Jan F.J., Chen M.C., Yeb. S.D. Jan F.J., Chiang C.H., Doong T.J., Chen M.C., Chung P.H., Bau H.J.; "Complete nucleotide sequence and genetic organization of papaya
PROSITE; PSS0096; 1Q; 2. Wyosin; Calmodulin-binding; Repeat; Colled coil; ArP-binding; Repeat; Colled coil; Alkylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                           90.0%; Score 27; DB 1; Length 1471; 83.3%; Pred. No. 2.5e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           72 ATP (POTENTIAL).
88 ALKYLATION (BY SIMILARITY).
98 ALKYLATION (BY SIMILARITY).
169343 MW; E79C0FE72B041E95 CRC64;
                                                                              MYOSIN HEAD-LIKE
                                                                                                       10 1.
10 2.
10 3.
10 4.
10 5.
COILED COIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ringspot virus RNA.";
J. Gen. Virol. 73:2531-2541(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                               824
8469
8469
1063
172
688
698
                                                                                                                                                                                                                                       938 106
1299 140
165 17
688 68
698 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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NCBI_TaxID=31731;
                                                                                                                                                                                                                                                                     DOMAIN
NP BIND
MOD RES
MOD RES
SEQUENCE
                                                                                                       DOMAIN
                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
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POLG PRSVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are

    {RNA}(N).
    CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own Cterminus, commonly in the sequence -Tyr-Xaa-Val-Gly-|-Gly, in the processing of the potyviral polyprocein.
    PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
    PTM: THE VIRAL THA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTECLYTIC PROCESSING REGULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.
    SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
    SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
    SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

                                                                                                                    the
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Coat protein, Polyprotein, Covalent protein-RNA linkage, Helicase,
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 kDa PROTEIN 2 (BY SIMILARITY).
GENOME-LINKED PROTEIN (BY SIMILARITY).
NUCLEAR INCLUSION PROTEIN A
                                                                   CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-TERMINAL PROTEIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HELPER COMPONENT PROTEINASE
(BY SIMILARITY).
PROTEIN P3 (BY SIMILARITY).
6 kDa PROTEIN 1 (BY SIMILARITY).
CYTOPLASMIC INCLUSION PROTEIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).

WUCLEAR INCLUGION PROTEIN B

(BY SIMILARITY).

COAT PROTEIN (BY SIMILARITY).

SIMILARITY).

SIMILARITY).

ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
E90CD7523AC5243D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001410; DEAD.
InterPro; IPR0014010; DEAD.
InterPro; IPR001500; Helicase_C.
InterPro; IPR001500; Peptidase_C4.
InterPro; IPR001592; Poty_Coat.
InterPro; IPR001592; Poty_Coat.
InterPro; IPR001592; Poty_Pl.
InterPro; IPR001095; RNA_Pol_PsD.
InterPro; IPR001095; RNA_Pol_PsD.
Pfam; PF00863; Peptidase_C4; I.
Pfam; PF00863; Peptidase_C4; I.
Pfam; PF00863; Peptidase_C4; I.
Pfam; PF00863; Peptidase_C4; I.
Pfam; PF00864; Peptidase_C4; I.
Pfam; PF00865; RNA_GP, RNA_DOl; Pfam; PF00868; RNA_GP, RNA_DOl; I.
Pfam; PF00868; RNA_GP, RNA_DOl; I.
Pfam; PR00869; RNA_GP, RNA_DOl; I.
PR00869; RNA_CP, RNA_DOL; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X67673; CAA47905.1; -.
EMBL; S46722; AAB23789.1; -.
EMBL; X67672; CAA47904.1; -.
PIR, JQ1899; JQ1899.
MEROPS; C04.009; -.
MEROPS; C05.001; -.
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1; 381040 P
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SEQUENCE
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SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
SPECIES=E.coli; STRAIN=0157:H7 / RIMD N. MINTE-2115621; Pubmed=11289796;
Hayashi T., Makino K., Ohnishi M., Muzata K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Muzata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Shinagawa H., "Complete genome sequence of enterchemorrhagic Escherichia coli "Complete genome comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
D
                                         Gape
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SPECIES=B.coli, STRAIN=06;H1 / CFT073 / ATCC 700928;
MEDLINE=22386234; PubMed=12471157;
MEDLINE=22386234; PubMed=12471157;
MEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mayhew H.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21074933, PubMed=1120653, Mau B., Glasner J.D., Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Groefai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grocheck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Melch R.A., Blattner F.R., "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V. Billey M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                         ..
o
 Length 3344;
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Science 277:1453-1474(1997).
                                       0; Indels
                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein yobf.
YOBF OR B1824 OR C2232 OR Z2869 OR ECS2534 OR SF1402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 90.0%; Score 27; DB 1; I
83.3%; Pred. No. 6.1e+02;
ive 1; Mismatches 0;
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SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
                                                                                                                                                                                                                 47
                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                 Escherichia coli,
Escherichia coli 06,
Escherichia coli 0157:H7, and
                                         Conservative
                                                                                                                                                                                                                 STANDARD;
Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                149 SVDLEY 154
                                                                                                                                                                                                                                                                                                                                                                                                        Shigella flexneri.
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                                                                              1 SVDVEY
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                                                                                                                                                                                             ECOLI
YOBF EC
P76265;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                   EMBL; U32811; AAC22968.1;
PIR; H64025; H64025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                      1 SVDVEY 6
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SLDIEY
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RACI DICDI
ID RACI DICDI
AC Q9GPR2;
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     SSSSSEE ** SS
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                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                        "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scort J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Wenter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.7%; Score 26; DB 1; Length 47; 100.0%; Pred. No. 11; o. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AE000276; AAC74894.1; -...
EMBL, AE016761; AAA56811.1; -...
EMBL, AE01540; AAA56813.1; -...
EMBL, AE015164; AAA4303.1; -...
EMBL, AE015164; AAA4303.1; -...
EMBL, AE015164; AAA4303.1; -...
PTR, AE0794; R5794.
PTR, H64943; H64943.
R COGGMEN; EG14882; YobF.
HYDOLHeeical protein; Complete proteome.
SEQUENCE 47 AA; 5212 MW; 54E439F3331D708F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypochetical protein H11323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: STRONG, TO E.COLI YCBG.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                  Gaps
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MEDLINE=21127961; PubMed=11222756;
Rivero F., Dislich H., Glockner, Noegel A.A.;
Rivero F., Dislich H., Glockner family of Rho-related proteins.";
The Distypstellum discoddum family of Rho-related proteins.";
Nucleic Acids Res. 29:1068-1079(2001).
-I- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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R HSSP; P15154; 1E96.
R DiccyDb; DD72727; rac1.
R InterPro; IPR003578; GTPase_Rho.
R InterPro; IPR003525; Small_GTP.
R InterPro; IPR004196; Ras trinsfrmug.
R InterPro; IPR00525; Small_GTP.
R Fam; P70071; ras; 1.
R WAART; SM00174; RAS; 1.
R TIGRFAMS; TIGR00231; small_GTP; 1.
R TIGRFAMS; TIGR00231; small_GTP; 1.
R PIND 59 63 GTP (BY SIMILARITY).
T NP_BIND 59 63 GTP (BY SIMILARITY).
T NP_BIND 119 122 GTP (BY SIMILARITY).
T NP_BIND 134 42 EFFECTOR REGION (POTENTIAL).
T LIPID 202 202 GERANYL-GERARYL (BY SIMILARITY).
SRQUENCE 205 AA; 22997 MW; F9EFDA31576C45CC CRC64;
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0
                                                                                                                                             Score 26, DB 1; Length 148;
Pred. No. 38;
2; Mismatches 0; Indels
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TIGR; H11323; -.
Hypothetical protein; Complete proteome.
SEQUENCE 148 AA; 17997 MW; F400CFE7A4958314 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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AAD16169.1;
BAB14399.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 SVEVEY 144
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
TRFP_MOUSE
ID _TRFP_MOUSE
                                                                                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ROXO;
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CAR RANK RANK FFF OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R Klaunner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Morer T., Max S.I., Wang J., Hsieh F.,

La stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morewan P.J., McKernan K.J., Malek J.A., Gunzardne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevohenko Y., Boniques S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Reneral A., Schein J.E., Jones S.J.M., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99134313; PubMed=9933582;
Xiao H., Tao Y., Roeder R.G.;
Xiao H., Tao Y., Roeder R.G.;
With human Part of Drosophila TRF-proximal protein is associated with an RNA polymerase II-SRB complex.";
J. Biol. Chem. 274:3937-3940(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Raku Y., Kodaira H., Kondo H.,
Takahashi M., Chiba Y., Ishida S., Mirakwa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.,
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May regulate transcription of class II genes through association with the RNA polymerase II-SRB complex.
-!- SUBUNIT: Component of an RNA polymerase II-SRB complex.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                       Q9H944; O95821; Q9Y429;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
TRF-proximal protein homolog.
                                                                                             212 AA
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MEDLINE=22388257; PubMed=12477932;
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                                                                                             STANDARD:
                                                                                                                                                                                                                                                                                                                  sapiens (Human)
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                                                                                          TRFP HUMAN
                             RESULT 20
THE HUMAN
TO PHUMAN
TO CHORD
DT 15-SEP
DN TRF-Pr
CO CO MAMMATANA
RA WATANA
RA RANA
RA SCHOBI
RA RANA
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EMBL; AK023092; BAB14399.1; -.
EMBL; AK053092; BAB14399.1; -.
EMBL; AL050196 (CAB4314.1; -.
EMBL; AL050196 (CAB431314.1; -.
GO; GO:0016251; F:general RNA polymerase II transcription factor; TAS.
GO; GO:0005515; F:protein binding; TAS.
GO; GO:0005515; P:regulation of transcription from Pol II pro. . .; TAS.
Transcription regulation; Nuclear protein.
CONFLICT 134 136 SAR -> VP (IN REF. 1).
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB 1; Length 212;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN REF. 1).
SAA7A39981EB1498 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i5-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
TRF-proximal protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6J; TISSUE-Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                206 207 M
212 AA; 23222 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.3%;
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HEM3 AERPE
Q9Y9J0;
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CARBOHYD
CARBOHYD
SEQUENCE
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HEM3_AERPE
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        STATE THE TENT THE TE
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REQUENCE FROW N.A.

STRAINE-CV. Columbia;

RA MEDIATE-21016720; PubMed=11130713;

RA Alanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

RA Fartmann B., Vallen G., Bloecker H., Perez-Alonso M., Obermaier B.,

RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomench P.,

RA Micker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,

RA Wicker D., Lorden K., Rater G., Bennes V.,

Wichelmann R., Kranz H., Woss H., Folland R., Barnat P., Nyakatura G.,

RA Wedelmann R., Kranz H., Yose H., Folland R., Barnat P., Nyakatura G.,

RA Worzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

ROTAR A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,

RA Mannhaupt G., Haase D., Schoen O., Bargues M., Liguori R., Vitale D.,

RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mowes H.-W.,

RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Johnkins J.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Walts A., Wu D., Peterson J., Van Aken S.,

RA Rase C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Sasamoto S., Kimura T., Idesawa K., Rawashina K., Kishida Y.,

RA Sasamoto S., Kimura T., Idesawa R., Massumoto C., Wada T.,

RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,

RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,

RA Watanabe A., Yamada M., Tabata S.,
                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Expansin-like 3 precursor (At-EXPL3) (Ath-ExpBeta-2.3).
EXPL3 OR AT3G45860 OR F16L2_170.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyra, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Rosidae, eurosids II, Brassicales; Brassicaceae, Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                     similarity).
SUBUNIT: Component of an RNA polymerase II-SRB complex (By
association with the RNA polymerase II-SRB complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.7%; Score 26; DB 1; Length 212; 83.3%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; Nuclear protein.
SEQUENCE 212 AA; 23192 MW; 88E116D0A9764438 CRC64;
                                                                                                                       similarity).
SUBCELLULAR LOCATION: Nuclear (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ245617; CAB53514.1; -. EMBL; AX043396; BAC31536.1; -. MGD; MGI:1929648; Trfp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 SVEVEY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SVDVEY 6
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ID EXL3 ARATH
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable porphobilingen deaminase (EC 4.3.1.8) (PBG)
(Hydroxymethylbilane synthase) (HYBS) (Pre-uroporphyrinogen synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=99310339; PubMed=10382966;
Kawarabayasi Y., Harkawa H., Yamazaki S., Haikawa Y.,
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S.-I., Ankai A., Kosugi H.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Makamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-1- FUNCTION: TETRAPOLYMERIZATION OF THE MONOPYRROLE PBG INTO THE
"Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXPANSIN-LIKE 3.

EXPANSIN-LIKE EG45.

EXPANSIN-LIKE CGB.

N-LINKED (GLCNAC.,) (POTENTIAL)

N-LINKED (GLCNAC.,) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5D8A2048FEA7C292 CRC64;
                                           Nature 408 820-822 (2000).

-!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
-!- SIMILARITY: Contains ! expansin-like EG45 domain.
-!- SIMILARITY: Contains ! expansin-like CBD domain.
-!- DATABASE: NAME=EXPANSIN homepage;
WWW="http://www.bio.psu.edu/expansins/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; T47536; T47536.
InterPro; IPR07112; Expan_endogl.
InterPro; IPR07112; Expan_endogl.
InterPro; IPR07113; Expan_Lol_pI.
InterPro; IPR07117; Expan_Lol_pI.
PR1875; PR01225; ExpanSmPAUX.
PRODOM; PD002179; Expan_Endogl.
PROSITE; PS50843; EXPANSIN_EGB; 1.
PROSITE; PS50843; EXPANSIN_EGB; 1.
PROSITE; PS50843; EXPANSIN_EGB; 1.
PROSITE; PS50843; EXPANSIN_EGB; 1.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 147 EX
161 243 EX
9 9 N-
102 102 N-
263 AA; 28559 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL162459; CAB82820.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
147
243
102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 VDVEY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VDVEY 6
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SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
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                                                                                                          EMBL; U39717; AAC71584.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma pneumoniae.
                                                                                                                                PIR; G64239; G64239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 SIDVQY 246
                                                                                                                                                                                                                                                                                                   Complete proteome.
NP BIND 45
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
ses 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae."
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P75242;
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                Query Match
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RUVB MYCPN
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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KEAIN-ATCC 33530 / G-37;

KEAIN-ATCC 33530 / G-37;

KEDINE-960263446; PubMed=7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Reischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Reischmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Sandl K.F., Hu P.-C., Lucier T.S.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403 (1995).

-I- FUNCTION: THE RUVA-RUVB COMPLEX IN THE PRESENCE OF ATP RENATURES

CRUCIFORM STRUCTURE IN SUPERCOILED DNA WITH PALINDROMIC SEQUENCE,

HOWOLOGOUS RECOMBINATION. RUVAB IS AN HELICASE THAT MEDIATES THE

HOLLIDAY JUNCTION MIGRATION. BY LOCALIZED DENATURATION AND

REANNBLING (BY SIMILARITY).

C. I- SUBUNIT: FORMS A COMPLEX WITH RUVA.
HYDROXYMETHYLBILANE PREUROPORPHYRINOGEN IN SEVERAL DISCRETE STEPS.

ANALAYTIC ACTIVITY: 4 porphobilinogen + H(2)0 =

hydroxymethylbilane + 4 NH(3).

COFACTOR: COVALENTLY BINDS A DIPYRROMETHANE COFACTOR TO WHICH THE

PORPHOPILINOGEN SUBUNITS ARE ADDED (BY SIMILARITY).

PATHWAY: PORPHYIN biosynthesis by the C5 pathway; fourth step.

SIMILARITY: BELONGS TO THE HMBS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%; Score 26; DB 1; Length 305; 100.0%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 AA; 33085 MW; 57C78EE934C2799B CRC64;
                                                                                                                                                                                                                                                                                                                                                                  Ptam; Prussuv, rocknocentry, Ptam; Pruss, Prosentry, Processes, 1.
Probom; PD002745; Porphobil deam; 1.
PROSITE; PS00533; PORPHOBILINOGEN DEAM; 1.
Porphyrin biosynthesis; Lyase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RUVB OR MG359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. ....
                                                                                                                                                                                                                                                            EMBL; AP000064; BAA81310.1; -.
PIR; F72456; F72456.
HSSP; P06891; 1PDA.
HAMAP; MF_00260; -; 1.
INTERPEO: 1PRO00860; Porphobil deam.
Pfam; PP01379; Porphobil_deam.
Pfam; PF01390; Porphobil_deam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
Les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDVEY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RUVB MYCGE
049425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fucies Acids Res. 24:4420-4449(1996).

-!- FUNCTION: THE RUYA-RUYB COMPLEX IN THE PRESENCE OF ATP RENATURES CRUCIFORM STRUCTURE IN SUPERCOLLED DNA WITH PALINDROMIC SEQUENCE, INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN HOMOLOGOUS RECOMBINATION. RUVAB IS AN HELICASE THAT MEDIATES THE HOLLIDAY UNKTION MIGRATION BY LOCALIZED DENATURATION AND REANNELING (BY SIMILARITY).

-!- SUBBUNT: FORMS A COMPLEX WITH RUVA.

-!- SIMILARITY: BELONGS TO THE RUVB PAMILY.
                                                                                                                                                                                                               TIGR; MG359; -... 1.

HAMAP; MF 00016; -.; 1.

HAMAP; MF 00016; -.; 1.

InterPro; IPR00359; AAA ATPase.

InterPro; IPR004605; RuvB.

Pfam; PR00046, AAA; 1.

SMART; SM00382; AAA; 1.

TIGRFAMS; TIGR00615; ruvB; 1.

TIGRFAMS; TIGR00615; ruvB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.7%; Score 26; DB 1; Length 307; llarity 66.7%; Pred. No. 83; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 52 ATP (POTENTIAL).
307 AA; 35000 MW; 376E5138279E396C CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Holliday junction DNA helicase ruvB.
RUVB OR MPNS36 OR MP306.
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InterPro; IPR003593; AAA_ATPase.
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h.

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SEQUENCE
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VT2_MYXVL
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MEDLINE=21608551; PubMed=11743194;
Medodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Mcodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L.,
Mourollo B., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Planagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.,
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens CS8.",
Science 294:232-2328(201).
C. - FUNCTION: FLIM IS ONE OF THREE PROTEINS (FLIG, FLIN, FLIM) THAT
SCIENCE 294:2323-2328(201).
C. - FUNCTION: FLIM IS ONE OF THREE PROTEINS (FLIG, FLIN, FLIM) THAT
COP THE BASAL BODY. THIS COMPLEX INTERACTS WITH THE CHEY AND CHEZ
CHEMOTAXIS PROTEINS, IN ADDITION TO CONTACTING COMPONENTS OF THE
MOTOR THAT DETERMINE THE DIRECTION OF FLAGELLAR ROTATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome of the natural genetic engineer Agrobacterium tumefaciens
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InterPro; IPR00359; AAA ATPase centr.
InterPro; IPR004605; RuvB.
Pfam; PR00004; AAA; 1.
SYART; SM00382; AAA; 1.
TIGRFAMs; TIGR00635; ruvB; 1.
DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Pahmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=97305159; PubMed=9161425;
Deakin W.J., Parker V.E., Loake G.J., Shaw C.H.;
"The Agrobacterium tumefaciens motor gene, moth, is in a linked cluster with the flagellar switch protein genes, fliG, fliM and
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobium/Agrobacterium group; Agrobacterium.
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                                                                                                                                                                                  POTENTIAL).
B1947D0C7AFFAF3A CRC64;
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28-FEB-2003 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, La
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                                                                                                                                                                                                                                                             86.7%; Score 26; DB
66.7%; Pred. No. 83;
iive 2; Mismatches
                                                                                                                                                                                       ATP
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35012 MW;
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Best Local Similarity bo...
4, Conservative
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241 SIDVQY 246
                                                                                                                                                            Complete proteome.
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(44457;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20032073; PubMed=10562494;
Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
Macaulay C., Willer D., Evans D., McFadden G.;
"The complete DNs sequence of myxoma virus.";
Virology 264:298-318(1999).
-I- FUNCTION, BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.
-I- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myxoma virus (strain Lausanne).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor soluble receptor precursor (Protein T2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.7%; Score 26; DB 1; Length 321;
66.7%; Pred. No. 87;
iive 2; Mismatches 0; Indels
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Interpro, IRROD543, SpoA.
Pfam; PF01052; SpoA.
Chemotaxis, Flagella, Flagellar rotation, Inner membrane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 157 G -> C (IN REF. 1).
160 160 E -> V (IN REF. 1).
321 AA; 34633 MW; D944CAE218C2D7B9 CRC64;
SUBCELLULAR LOCATION: Inner membrane-associated. SIMILARITY: BELONGS TO THE FLIM FAMILY.
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                                                                                                                                                                                                                                                                                                         EMBL; AE009025; AAL41578.1; ALT_INIT.
EMBL; AE007990; AAK86373.1; -.
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CONFLICT 157
CONFLICT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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60 AIDVEY 65
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P29825;
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Morgan J.G., Holbrook N.J., Crabtree G.R.;
"Nucleotide sequence of the gamma chain gene of
conserved intronic sequences.";
Nucleic Acids Res. 15:2774-2776(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
01-PEB-1996 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annocation update)
Fibrinogen gamma chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 AA.

    -i- SIMILARITY: Belongs to the recA family.

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or send an email to license@isb-sib.ch).
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MEDLINE=83129318; PubMed=6897622;
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66.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
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112 SLDIEY 117
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R EMBL; AF170726; AAF15446.1; -
R EMBL; AF3729; CAA01680.1; -
R EMBL; AA573729; CAA01680.1; -
R ETR; A40566; GQVZML.
R PIR; A40566; GQVZML.
R PIR; A4050020; TNFR_C6.
R Pfam; PF000200; TNFR_C6.
R Pfam; PR00200; TNFR_C6.
R PROSITE; PS00052; TNFR_NGFR_1; 2.
R RAAFT; SM00208; TNFR_NGFR_1; 2.
R ROSITE; PS00052; TNFR_NGFR_1; 2.
R RCSITE; PS00050; TNFR_NGFR_1; 3.
R RCSITE; PS00050; TNFR_NGFR_2; 3.
R RCSITE; PS00050; TNFR_NGFR_2; 3.
R RCSITE; PS00050; TNFR_NGFR_2; 2.
R RCSITE; PS00050; TNFR_NGFR_2; 3.
R RCSITE; 
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MEDLINE=97251810; PubMed=9097419;

Agarvey P., Rince A., Hill C., Fitzgerald G.F.;

MEDLINE=97251810; PubMed=9097419;

MEDLINE=97251810; PubMed=9097419;

I deartification of a recA homolog (recALP) on the conjugative lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence plasmid pNP40: evidence plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence plasmid pNP40: evidence of a role for lactococcal phage phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence of a role for lactococcal phage phage resistance plasmid pNP40: evidence of a role for lactococcal phage resistance plasmid pNP40: evidence plasmid pNP40: evidence plasmid pNP40: evidence plasmid pNP40: evidenc
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NCHI_TaxID=1360;
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TUBE-CYS 2.

TUBE-CYS 3.

TUBE-CYS 4.

BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RecA protein, plasmid (Recombinase A) (recalP).
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  send an email to license@isb-sib.ch)
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                                                       EMBL; M95181; AAA46632.1; -.
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Best Local Similarity 66.7.,
A; Conservative
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287 NVDIEY 292
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AC Q59486;
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MEDLINE=84194000; PubMed=6232608;
POWIKES D.M., Mullis N.T., Comeau C.M., Crabtree G.R.,
Fowlate D.M., Mullis N.T., Comeau C.M., Crabtree G.R.,
Fortential basis for regulation of the coordinately expressed
fibrinogen genes: homology in the 5' flanking regions.";
Froc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
-I- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
EMBL; U36837; AAB52384.1; -.
HAMPP; WF 00208; -.
HAMPP; WF 002089; -.
InterPro; IPR001553; RecĀ.
R InterPro; IPR001553; RecĀ.
R Pfam; PR00154; recA; 1.
R PROMO; PR000229; RecA; 1.
R PROSTTE; PS00124; RECA; 1.
R PROSTTE; PS0162; RECA 1; 1.
R PROSTTE; PS0162; RECA 2; 1.
R PROSTTE; PS0162; RECA 2; 1.
R PROSTTE; PS0163; RECA 2; 1.
R PROSTTE; PS0163; RECA 3; 1.
R PROSTER; PS0163; RECA 3; 1.
R PROST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crabtree G.R., Kant J.A., "Organization of the rat gamma-fibrinogen gene: alternative mRNA splice patterns produce the gamma A and gamma B (gamma ') chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rat fibrinogen:
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Pred. No. 93;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY).
; F9D4BCCCEA69EAB5 CRC64;
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey B.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                                                                                                                                                                                                                                                                                                                XTAIN=H3TRY,

X FEBLINE=98295987; PubMed=9634230;

X MEDLINE=98295987; PubMed=9634230;

X Goldon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Goldon S.V., Eiglmeier K., Barkmu D., Chillingworth T., Connor R.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Woule S., Murphy L.,

A Nutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Sulston J.B., Taylor K., Whitchead S., Barrell B.G.;

A Sulston J.B., Taylor K., Whitchead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last amotation update)
GLYSON RY2357C ON MT2426 ON MTCY27.23 ON MTCY98.26
MYCObacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                     STATE BEART BEART BEART BEART COCCOCCOCCOCCOCC STATE BEART B
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                                                                                                                                                 NAMESCALMANA,

ISOID-POZGEO.2; SEQUENCE-VSP 001538, VSP 001539;

ISOID-POZGEO.2; SEQUENCE-VSP 001538, VSP 001539;

MISCELLANBOUS. CONVERSION OF FIRRINOGEN TO FIRRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIRRINOPERPILES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CAPALYZES THE
EPSILON (GAMMA-GLUTAMYL) LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
(STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
AGGREGATION.
SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH GAMMA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH GAMMA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH BETA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH ALPHA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH BETA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH GAMMA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH GAMMA CHAIN)
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00514; FIBRIN_AG_C DOMAIN; 1.
Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma; Alternative splicing; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIBRINOGEN GAMMA CHAIN.
INTERCHAIN (WITH GAMMA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (In isoform Gamma-A) /FIId=VSP_001539.
                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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                                                                                       Event=Alternative splicing; Named isoforms=2;
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BY SIMILARITY.
                                                                                                                                 IsoId=P02680-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, J00733; -; NOT_ANNOTATED_CDS.
EMBL, J00734; -; NOT_ANNOTATED_CDS.
EMBL, X05860; CAA29289.1; -.
EMBL, X05861; CAA29289.1; -.
EMBL, X0137; AAA98626.1; -.
FIR, A90828; FGRTGA.
HSSP; POZ679; JFID.
Interpro; IPRO2181; Fibrinogen_C, FEm; PRO0147; fibrinogen_C; SWART; SM00186; FBG; 1.
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365
437
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352
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DISULPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 295209; CAB08466.1; -

REMBL; AE007082; AAK46720.1; -

REMBL; AE007082; AAK46720.1; -

REMBL; POSSES; D70585.

REMSP; PS6206; 1ATI.

RESP, PS6206; 1ATI.

RESP, PS6206; 1ATI.

RESP, PS6206; 1ATI.

RESP, PS6206191; RNA-Synt 2b.

RESP, PS6206195; RNA-Synt 2b.

RESP, PS6206195; RNA-Synt 2b.

RESP, PS6206195; RNA-Synt 2b.

RESP, PS6206195; RNA-Synt 2b.

REM; PR01043; RNA-Synt Gdly.

REM; PR01044; RNA-S
laboratory strains.";
Submitted (AFR-2001) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
                                                                                                                                                                                                                            + glycyl-tRNA(Gly).
-- SUBUNIT: Homodimer (By similarity).
-- SUBCELLULAR LOCATION: Cycoplasmic.
-- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 AA; 52937 MW; E8BDCE20B65538F7 CRC64;
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SEQUENCE 463 AA
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Gaps

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86.7%; Score 26; DB 1; Length 445; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels

86.78;

5; Conservative

VDVEY 444 2 VDVEY 6

440

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Local Similarity

Query Match Best Loca Matches

RESULT 31

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526 AA.
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                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                 SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001709; AAD35365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.7%;
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Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B72398; B72398.
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084786;
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SYK_CHLTR
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                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                               STRAINTCI / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Where complete sequence of the Pyrococcus furiosus genome.";
Submitted (EBE-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes amidations at positions B. D. E, and G on adenosylcobyrinic A,C-diamide. NH(2) groups are provided by glundamine, and one molecule of ATP is hydrogenolyzed for each amidation (By similarity).
-!- PATHWAY: Cobalamin biosynthesis.
-!- SIMILARITY: BELONGS TO THE COBB/COBQ FAMILY. COBQ SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBI_TaxID=2336;
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 Length 463;
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Query Match 86.7%; Score 26; DB 1; Length 463
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26; DB 1; Length 483
Pred. No. 1.3e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMDA, M. 20028, -; 1.
HAMDA, M. 20028, -; 1.
INTERPRO, IPR002586; CbiA.
InterPro; IPR004459; CobQ.
Pfam; PF01656; CbiA; 1.
TIGRPAM; TIGR00313; CobQ; 1.
Cobalamin biosynthesis; Complete proteome.
Cobalamin biosynthesis; Complete proteome.
Cobalamin biosynthesis; Complete proteome.
                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cobyric acid synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARAA_THEMA STANDARD; E Q9WYB3; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last seques 28-FEB-2003 (Rel. 41, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE010154; AAL80425.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.78;
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Best Local Similarity 66.,
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                    Pyrococcus furiosus.
                                                                                                 268 TVDIEY 273
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471 SIDVDY 476
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                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2261;
                                                                  1 SVDVEY
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                                                                                                                                                                                                                                                                                 COBQ OR PF0301
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                                                                                                                                                                                COBQ PYRFU
QBU3Z8;
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ARANTHEMA
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DT 28-FEB
DT 38-FEB
ON 28-FEB
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Science 282:754-759(1998).
-!-CATALYITC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate + L-lysyl-tRNA(Lys).
-!-COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
-!-SUBUNIT: Homodimer (By similarity).
-!-SUBCLEULAR LOCATION: Cytoplasmic.
-!-SUMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Lihher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lygyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
LYSS OR CT781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                     nature 399:323-323(1593).
-!- CATALYTIC ACTIVITY: L-arabinose = L-ribulose.
-!- PATHWAY: L-arabinose catabolism; first step.
-!- SIMILARITY: Belongs to the arabinose isomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 1; Length 496;
Pred. No. 1.4e+02;
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HAWAP; MF 00519; -; 1.
HAWAP; MF 00519; -; 1.
InterPro; IPR003762; Lara isomerase.
Pfam; PF02610; Arabinose Tsome; 1.
ProDom; PD018364; Lara isomerase; 1.
ProDom; PD018364; Lara isomerase; 1.
Isomerase; Arabinose catabolism; Complete proteome.
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PIR, E74472; E71472.

BR HSAP, P14825; 1210.

BR HSAP, P14825; 1210.

BR InterPro; IPR004364; LRNA-synt 2.

BR InterPro; IPR004365; LRNA-synt 2.

BR InterPro; IPR004365; LRNA-synt 2.

BR InterPro; IPR004365; LRNA-synt 2; 1.

BR InterPro; IPR004355; LRNA-synt 2; 1.

BR InterPro; IPR004355; LRNA-synt 2; 1.

BR InterPro; IPR004365; LRNA-synt 2; 1.

BR MAGNESIUM 1 AND 2 (BY SIMILARITY).

BR MAGNESIUM 1 AND 2 (BY SIMILARITY).

BR AA: 60106 MW; BEAE8A47DDDDD41C CRC64;
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ö Gaps ; 0 86.7%; Score 26; DB 1; Length 526; 83.3%; Pred. No. 1.5e+02; iive 1; Mismatches 0; Indels Local Similarity 83.3 nes 5; Conservative Matches

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30-WAY-2000 (Rel. 39, Created)
34-NAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
UVRABC system protein C (UvrC protein) (Excinuclease ABC subunit C) Mycoplasma bovis. Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma. STANDARD; UVRC MYCBV 084898; 

STRAIN=PG45; MEDLINE=98329280; PubMed=9664578; SEQUENCE FROM N.A. NCBI\_TaxID=28903;

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). -!- SIMILARITY: Belongs to the uvrc family. -!- SIMILARITY: Contains 1 UVR domain.

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ö (See http://www.isb-sib.ch/announce/ Gaps | HAMAP, WF 00203; ALCOSONIA, ALC . 1: Indels SEQUENCE 571 AA; 66463 MW; 717DA202CA50DCE3 CRC64; 86.7%; Score 26; DB 1; I 83.3%; Pred. No. 1.6e+02; 0; Mismatches entities requires a license agreement (Sons send an email to license@isb-sib.ch). UVR. EMBL; AF003959; AAC32309.1; Local Similarity 83.3 nes 5; Conservative 219 1 SVDVEY 6 184 Query Match DOMAIN 요

409 SADVEY 414

Haematobia irritans exigua (Buffalo fly). Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Haematobia. 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
08-RDB-2003 (Rel. 41, Last annotation update)
Anglotenain-converting enzyme precursor (EC 3.4.15.1) (Dipeptidyl carboxypeptidase I) (Kininase II). STANDARD; NCBI\_TaxID=34678; ACE HAEIE Q10715; 

WEDLINE=96215437; PubMed=8647080;
WEDLINE=96215437; PubMed=8647080;
WHIJFfels G.L., Fitzgerald C., Gough J., Riding G.A., Elvin C.,
WHIJFfels G.L., Fitzgerald C., Gough J., Riding G.A., Elvin C.,
WHIJFFELS G.L., Fitzgerald C., Gough J., Riding G.A., Elvin C.,
WHIJFFELS G.L., Fitzgerald C., Gough J., Riding G.A., Elvin C.,
WHILARLY G.L., Fitzgerald C., Gough J., Riding G.A., Elvin C.,
WHILARLY G.L., Fitzgerald C., Gough J., Riding G.A., Elvin C.,
WHILARLY G.L., GOUGH J., Riding G.A., Elvin C., and XDD is neither
Oligopeptide-|-Xaa-Xbb, When Xaa is not Pro, and XDb is neither
Oligopeptide-|-Xaa-Xbb, When Xaa is not Pro, and XDb is neither
C.-- COPACTOR: Binds 1 zinc ion (By similarity).
C.-- COPACTOR: Binds 1 zinc ion (By similarity).
C.-- SIMILARLY: EXPRESSED IN THE COMPOUND GANGLION AND IN THE
POSTERIOR REGION OF THE MIDGUT.

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Mech. Dev. 51:157-168(1995).
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Cornell M.J., Coates D., Isaac R.E.;
"Characterisation of putative Drosophila angiotensin converting enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Canton-S;
MEDLINE=96028519; PubMed=7547464;
Tatel K., Cai H., Ip Y.T., Levine M.;
"Race: a Drosophila homologue of the angiotensin converting enzyme.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiotensin-converting enzyme precursor (EC 3.4.15.1) (Dipeptidy) carboxypeptidase I) (Kininase II). ANCE OR RACE OR BG:DS08220.3 OR CG8827.
                                                                                          InterPro; IPR001548; Peptidase M2.
InterPro; IPR06025; Zn MTpepdse.
Pfam: PF01401; PE01019.
PROINTS; PR00791; PEPDIPTAREA.
ProDom; PD004184; Peptidase M2; 1.
PROSINE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
                                                                                                                                                                                                                                                                                              ZINC (CALLERITY).

BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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Bukaryota, Merazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26; DB 1; Length 611;
Pred. No. 1.7e+02;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACE_DROME STANDARD; PRT; 615 AA. 010714; 027572; 09NE4; 09TX66; 09VJV3; 01-NOV-1997 (Rel. 35, Created) PFEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
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  send an email to license@isb-sib.ch)
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Biochem. Soc. Trans. 21:243-243(1993).
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                                    EMBL; L43965; AAA70427.1; -.
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368
371
                                                          PIR; S65472; S65472.
MEROPS; M02.003; -.
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531
611 AA;
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REPRINEMES FROM N.A.

REMAINTER-9440301. PubMed-1047107; Lewis S.E., Blazej R.G., Davis T., Amburner M., Mista S., Rooke J., Lewis S.E., Blazej R.G., Davis T., Amburner M., Mista S., Rooke J., Lewis S.E., Blazej R.G., Davis T., Amburner M., Mista S., Rooke J., Lewis S.E., Blazej R.G., Davis T., Amburner M., Mista S., Rooke J., Lewis S.E., Shandon G., Amburner M., Mista M., Mista M., Mista M., Amburner M., Amburner M., Mista M., Mist
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SEQUENCE FROM N.A.
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                                                                                                                  Kanoh
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                                                                                                                                                                      EMBL; U25544; AAB02171.1; -.

REMBL; U34599; AAC46902.1; -.

REMBL; AE003641; AAF4834.1; -.

REMBL; AE003641; AAF83353.2; -.

REMBL; AZ061129; AAL28677.1; -.

REMBL; AZ060129; AAL2867.1; -.

REMBL; AZ060129; AZ0601
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SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
MEDLINE=21534324; Pubmed=11676924;
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
WAYG -> GPMR (IN REF. 4).
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LOC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).
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C -> S (IN REF. 4).

G -> A (IN REF. 3).

I -> T (IN REF. 5, 6 AND 7).

V -> E (IN REF. 1).

S -> A (IN REF. 1).

S -> A (IN REF. 1).

S -> T (IN REF. 1).

S -> T (IN REF. 1).

A -> R (IN REF. 4).

A -> R (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
             SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              096TL7; Q9UTM1; Q9UU15; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) DNA-binding protein rapl. aspl. 08-RB1 OR SPE1779 40.2. Schlzosaccharomyces pombe (Fission yeast).
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THROUGHOUT EMBRYOGENESIS
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nes 5; Conservative
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RAPI_SCHPO
DT 28-FEB-DT 12-SEP-DT 12-SEP
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An Chikashiga Y. Himacka Y. Bimacka Bimacka
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NCBI_TaxID=10090;
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P59470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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   SO THE WAR BRANK B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the Bacillus subtilis chromosome region between
the serA and kdg loci cloned in a yeast artificial chromosome.";
Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                     Length 693;
                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                     693 AA; 79526 MW; 77C5070697D1A9CF CRC64;
                                                                                                                                                                                  Score 26; DB 1;
Pred. No. 2e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
-1- SIMILARITY: BELONGS TO THE HELICASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
InterPro; IPR001357; BRCT.
PROSITE; PS50172; BRCT; I.
DNA-binding; Telomere; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
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MEDLINE=96349105; PubMed=8760912;
                                                                                               BRC
                                                                                                                                                                              Match 86.7%;
Local Similarity 66.7%;
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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249 SIDVDY 254
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                                                                                                                                                                                                                                                                                                              1 SVDVEY 6
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PS0830;
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RE STRAINGES181/6131 TROM NA.

RE ORGARAXI Y. FULTON M. KASHKAWA T., Adachi J., Bono H., Kondo S.,

RA OKARAXI Y. FULTON M., KASHKAWA T., Adachi J., Bono H., Kiyosawa H.,

RA BAdarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Badarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baladarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Bala R., Dragani T.A., Fletcher C., Corbani L.E., Cousins S.,

RA Bala R., Dragani T.A., Fletcher C.F., Forrest A., Bracel K.S.,

RA Gasterland T.A., Gariboldi M., Glasi C., Godzik A., Gough J.,

RA Kamai H., Kawaju H., Kawasawa Y., Kedziereki R.M., Xing B.L.,

RA Kamai A., Kawaji H., Kawasawa Y., Kedziereki R.M., Xing B.L.,

RA Magott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magoshima T., Numara K., Okido T., Pavan W.J., Pertea G., Pesele G.,

RA Rayasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sultana R., Fakenaka Y., Taylor M.S., Taesdale R.D., Tomita M.,

RA Verardo R., Magner L., Mahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Willing L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yana Z. Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 1; Length 749;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Hydrolase; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84589 MW; 3F653EFA8EC3A7EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                       EMBL; 299115; CAB14139.1; -.
PIR; B69941; B69941.
Subtilist; BG11451; YprA.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                    EMBL; L47838; AAB38468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
NP BIND 76
SITE 185
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                   STRAIN=KI2 / MG1655;
MEDLINE=77426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997)
         16-OCT-2001 (Rel. 40, Last sequence update)
28-RBB-2003 (Rel. 41, Last annotation update)
Hypothetical protein yliE.
YLIE OR B0833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                     Escherichia coli
                                                                                                                                                                                                                                 NCBI_TaxID=562;
            RR SEQUENCE OF 552-756 FROM N.A.

SEQUENCE OF 552-756 FROM N.A.

STRAIN=C57BL/6J; TISSUE=Mammary gland;

RX ALTAUSDET TISSUE=Mammary gland;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Attasher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Attasher R.D., Collins F.S., Magner L., Shemmen C.M., Schuler G.D.,

RA Attasher R.D., Collins R., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Bras S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA, Roback S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RA, Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gubbs R.A.,

RA, Richards S., Worley K.C., Hale S., Garcia A.M., Gabb J.J., Hulyk S.W.,

RA, Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakseley R.M., Touchman J.W., Green B.D., Dickson M.C.,

RA Blakseley R.W., Touchman J.W., Green B.D., Myers R.W.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schahu J.E., Jones S.J.M., Marra M.A.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RT "Generation and initial analysis of more than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acadependences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-I- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates (By similarity).

C. I- CAPPLAYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {RNA}(N).
-!- SUBUNIT: RNA polymerase III consists of about 15 different
subunits. This subunit is the second largest component of RNA
polymerase III (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AK039366; BAC30327.1; -.
EMBL; BC044796; AA44796.1; -.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
Zinc-finger; Nuclear protein.
ZN_FING 703 718 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 756;
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551 552
756 756 756
756 AA; 85062 MW; 336763B7CEBBAFB8 CRC64;
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Best Local Similarity 66.7.
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 782 AA, 90048 MW, 608DFB0068611DFB CRC64,
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83.3%; Pred. No. 2.3e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
POLB OR APEZ098.
                                                                                                                                                                                                                                     PIR; A64821; A64821.
EccGene; EG13476; yliE.
InterPro; PR001633; EAL.
Fram; PP00563; EAL; 1.
SWART; SM0052; DUF2; 1.
PROSITE; RS50883; EAL; 1.
Hypothetical protein; Complete proteome.
DOMAIN.
527 781
                                                                                                                                                                       EMBL; AE000185; AAC73920.1; -.
EMBL; D90721; BAA35528.1; -.
EMBL; D90722; BAA35536.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.30,
Local Similarity 83.30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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ID DPO2_AERPE
AC 093746;
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YLIE ECOLI 1D YLIE ECOLI STANDARD; 1D 7LIE ECOLI STANDARD; DT 16-OCT-2001 (Rel. 40, Created)

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MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816; PubMed=11997336;

A Ghen Y., Xue Y., Xu X., Xuaz., Xuan Z., Hu S., Dong W., Yang J.,

A Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

A Complete Sequence of T., tengcongensis genome.";

Genome Res. 12:689-700(2002).

C CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +

Genome Res. 12:689-700(2002).

C CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +

Genome Res. 12:689-700(2002).

C CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +

Genome Res. 12:689-700(2002).

C CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +

Genome Res. 12:689-700(2002).

C CATALYTIC Selection of two alpha and two beta chains (By similarity).

C C SUBMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain family. Subfamily 1.

C C SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Metal-binding; Magnesium; RNA-binding; tRNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRNA-BINDING.
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (VIA CARBONYL OXYGEN)
                                             Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.7%; Score 26; DB 1; Length 794; 100.0%; Pred. No. 2.3e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
F9179929B0461A7F CRC64;
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase beta chain) (PheRS). PHET OR TTE1689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 43
VP3 BTV10
ID VP3 BTV10
ID VP3 BTV10
AC P12435,
DT 01-0CT-1989 (Rel. 12, Created)
DT 01-0CT-1989 (Rel. 12, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00283; -; 1.
InterPro; IPR005146; B3 4.
InterPro; IPR005147; B5.
InterPro; IPR005121; Rdx-AntiCB.
InterPro; IPR004532; PheT_bact.
InterPro; IPR002547; tRNA_bind.
Pfam; PF03484; B5; 1.
Pfam; PF03484; B5; 1.
Pfam; PF03189; TRNA_bind; 1.
Pfam; PF03189; TRNA_bind; 1.
IGRFAMS; IIGR0472; pheT_bact; 1.
PROSITE; PS50886; TRBD; 1.
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Best Local Similarity 100....
Best Local Similarity 100...
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457
463
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467 4
794 AA;
                                                                                                                                                  SEQUENCE FROM N.A.
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457
463
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SEQUENCE
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                                                                                        STRAIN=K1;
Ishino Y., Cann I.K.;
"Isolation of the genes encoding two alpha-like DNA polymerases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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EMBL; AB017501; BAA75663.1; -...

PIR; P72515; E72515.

HISP; P56689; 1750.

InterPro; IPR006172; DNA_DOl_B -...

InterPro; IPR006131; DNA_DOl_B -...

InterPro; IPR0045131; DNA_DOl_B -...

InterPro; IPR0045131; DNA_DOl_B -...

Pfam; PF03104; DNA_DOl_B; 1...

Fram; PF03104; DNA_DOl_B; 1...

SMART; SM0486; P01Bc_1...

IGR0592; DNA_DOl_B: 1...

RROSITE; P500116; DNA_POLYMERASE B; 1...

TGRAMB; TIGR00592; DNA_POLYMERASE B; 1...

Transferase; DNA_directed DNA_POLYMERASE B; 1...

Transferase; DNA_directed DNA_POLYMERASE D, 1...

Transferase; DNA_directed DNA_POLYMERASE D, 1...
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KIGERVTLEWWQIG -> R (IN REF. 1).
E -> Q (IN REF. 1).
LRILQY -> SAHTSSN (IN REF. 1).
T -> I (IN REF. 1).
T -> I (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 26; DB 1; Length 784; 100.0%; Pred. No. 2.38+02; ive 0; Mismatches 0; Indels
 Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                             Aeropyrum pernix.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
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                    Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56636;
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Best Local Similarity 100....
S; Conservative
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355
355
754
763
784 AA;
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                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SYPB THETN
ID SYPB THETN
AC QGR9C7,
DT 15-SEP-2003
DT 15-SEP-2003
DT 15-SEP-2003
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CONFLICT
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hwang G.-Y., Xiang M., Li J.K.-K.;
"Analyses and conservation of sequences among the cognate L3 segments of the five United States bluetongue viruses.";
Virus Res. 32:381-389(1994).
-I-FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
-I-SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 26; DB 1; Length 901; 66.7%; Pred. No. 2.6e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.7%; Score 26; DB 1; Length 901; 66.7%; Pred. No. 2.6e+02; ative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    901 AA; 103405 MW; 2C81F5D7CA304D0D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VP3 core protein (Major inner capsid protein)
S3 OR L3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bluetongue virus (serotype 13 / isolate USA).
Viruses, dsRNA viruses, Reoviridae, Orbivirus.
NCBI_TaxID=33717,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=94360628; PubMed=8079518;
                                                                                                                                                                                                                                                                InterPro; IPR002614; Orbi VP3.
Pfam; PF01700; Orbi VP3; I.
ProDom; PD004438; Orbi VP3; I.
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Pfam; PF01700; Orbi VP3; 1.
ProDom; PD004438; Orbi_VP3; 1.
                                                                                                                                                                                                           EMBL; L19968; AAA42846.1; -.
HSSP; P56582; 2BTV.
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Best Local Similarity 66.73
Best Local 4; Conservative
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454 TIDVEY 459
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SEQUENCE 90
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VP3_BTV13
ID VP3_BTV13
AC Q65750;
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SEQUENCE FROM N.A.
BEDLINE=90345726; PubMed=2166648;
Roy P., Marshall J.J.A., French T.J.;
Structure of the bluetongue virus genome and its encoded proteins.";
Curr. Top. Mcrobiol. Immunol. 162.43-87(1990).
-!- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
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SEQUENCE FROM N.A.
MEDLINE=94360628; PubMed=8079518;
MEDLINE=94360628; PubMed=8079518;
Hwang G.-Y., Xiang M., Li J.K.-K.;
"Analyses and conservation of sequences among the cognate L3 segments of the five United States bluetongue viruses.";
virus Res. 32:381-389(1994).
-!- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
                                                                                                                                                                                                        MEDINE=86046560, PubMed=2998117;
Adhash H., Purdy M.A., Roy P.;
"The complete sequence of bluetongue virus serotype 10 segment 3 it predicted VP3 polypeptide compared with those of BTV serotype
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                                                    S3 OR L3.
Bluetongue virus (serotype 10 / isolate USA).
Viruses; dsRNA viruses; Reoviridae; Orbivirus.
NCBI_TaxID=10900;
15-DEC-1998 (Rel. 37, Last annotation update) VP3 core protein (Major inner capsid protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bluetongue virus (serotype 11 / isolate USA).
Viruses; dsRNA viruses; Reoviridae; Orbivirus.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VP3 core protein (Major inner capsid protein)
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InterPro, IPR002614, Orbi VP3.
Pfam, PF01700, Orbi VP3, 1.
ProDom; PD004438, Orbi VP3, 1.
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                                                                                                                                                                                                                                                                                                                                          Virus Res. 3:181-190(1985).
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les 4; Conservative
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454 TIDVEY 459
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SEQUENCE FROM N.A.
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SEQUENCE 90
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VP3 BTV11
Q65749;
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Matches
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VP3 BIV11
VP3 BIV11
DT 15-DE

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X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

X FILL

X Grimes J.M., Burroughs J.N., Gouet P., Diprose J.M., Malby R.,

Zientara S., Mertens P.P., Stuart D.I.; The atomic structure of the bluetongue virus core.";

II. Nature 395.470-478 (1998).

II. Nature 395.470-478 (1998).

-1 FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CABSID OF THE VIRUS.

-1 SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.

DB3, 2BTV; 09-288P-98.

R InterPro; IPR002614; Orbi_VP3.

R Ffam; PF01700; Orbi_VP3; I.

NR Frobom; PD004438; Orbi_VP3; I.

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Core protein; 3D-structure.
         orbivirus isolates.";
Virus Res. 7:169-183(1987).
-!- FUNCTION: THE VP3 PROTEIN (WITH VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
Interpro; IPR002614; Orbi VP3.
Pfam; PF01700; Orbi VP3; I.
ProDom; PD004438; Orbi VP3; 1.
South Africa and the United States of America, and with other
                                                                                                                                                                                                     86.7%; Score 26; DB 1; Length 901; 66.7%; Pred. No. 2.6e+02; ive 2; Mismatches 0; Indela
                                                                                                                                                                        901 AA; 103205 MW; 12312208188C1206 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bluetongue virus (serotype 1 / isolate South Africa).
Viruses; dsRNA viruses; Reoviridae; Orbivirus.
VGBI_TaxID=10905;
                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
VP3 core protein (Major inner capsid protein)
                                                                                                                                                                                                                                                                                                                                                                                    901 AA.
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Best Local Similarity 66./°,
Best A; Conservative
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SEQUENCE 90
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P56582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-82242823; PubMed=2889873;
MEDLINE-82242823; PubMed=2889873;
ROY P., Purdy M.A., Petre G., Rao C.D.;
RCloning and nucleotide sequencing of bluetongue virus genomes.";
Prog. Clin. Biol. Res. 178:363-370(1885).
--- PUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
--- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bluetongue virus (serotype 1 / isolate Australia).
Viruses, dsRNA viruses; Reoviridae; Orbivirus.
NCBI_TaxID=10904;
                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                     VP3 core protein (Major inner capsid protein)
S3 OR L3.
                                                                                                                                    Bluetongue virus (serotype 17 / isolate USA).
Viruses; dsRNA viruses; Reoviridae; Orbivirus
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                           901 AA
                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=84292453; PubMed=6206235;
Purdy M.A., Petre J., Roy P.;
"Cloning of the bluetongue virus L3 gene.";
J. Virol. 51:754-759(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002614; Orbi VP3.
Pfam; PF01700; Orbi VP3; I.
ProDom; PD004438; Orbi VP3; 1.
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EMBL; M32722; AAA42839.1; -.
PIR; A04148; P3XR17.
HSSP; P56582; 2BTV.
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Best Local Similarity 66.73,
A: Conservative
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                          VP3_BTV17
P03539;
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RESULT 47
VP3 BTV1A
DD BAC P2060
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DT 15-DE
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RRN (SI)
RR SEQUE
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RT HAE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94360628; PubMed=8079518; Hwang G.-Y., Xiang M., Li J.K.-K.; Hwang G.-Y., Xiang M., Li J.K.-K.; Analyses and conservation of sequences among the cognate L3 segments of the five United States bluetongue viruses."; Virus Rse. 32:381-389(11994).
-!-FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
-!-SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
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86.7%; Score 26; DB 1; Length 901;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
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VP3 BTV2A

AC 065748;
DT 15-DEC-1998 (Rel: 37, Created)
DT 15-DEC-1998 (Rel: 37, Last sequence update)
DF 23 OR L3.
ON L3.
ON L3.
DB Latternous (Serotype 2 / isolate USA).
ON Viruses; derNA viruses; Recviridae; Orbivirus.
ON NCBI_TaxID=10907;
RM MEDLINE=94360628; PubMed=8079518;
RM SNESS-PROT entry is copyright. It is produced the SWiss Institute of Bioinformatics a the European Bioinformatics Institutions as its copyright and this statement is not removed. Usage CC between the SWiss Institutions as long as its modified and this statement is not removed. Usage CC mend an email to license@isb-sib-ch).
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DR RNSD: PEGSE2; ZBTV.
DR RNSSP: PEGSE2; ZBTV.
DR RNSSP: PEGSE2; ZBTV.
DR RNSSP: PEGSE2; ZBTV.
DR RNSP: PEGSE2; ZBTV.
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SEQUENCE OF 751-1133 FROM N.A.

SEGUENCE OF 751-1133 FROM N.A.

TISSUE-Teratocarcinoma;

A ISOBAT T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A ISOBAT T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H., Sugawara M.,

A Magatsuma M., Hospiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Minomico J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Ninomiya K., Iwayanaqi T.;

"NEDO human cDNA sequencing project.";

RI "NEDO human cDNA sequencing project.";

CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription

CC -!- FUNCTION: DNA using the four ribonucleoside triphosphates as TISSUENCE FROM N.A.

TISSUEMUSCIE;
MEDLINE-2388257; PubMed=12477932;
MEDLINE-2388257; PubMed=12477932;
MEDLINE-2388257; PubMed=12477932;
MEDLINE-2388257; PubMed=12477932;
MISCALI S., Feingold E.A., Grouse L.H., Derge J.G.,
Malschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Heid E.,
Matchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Caraninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.W., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Milalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Milting W., Molley M., Scheurz D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
McGeneration and initial analysis of more than 15,000 full-length "Characterization of human RNA polymerase III identifies orthologues for Saccharomyces cerevisiae RNA polymerase III subunits."; Mol. Cell. Biol. 22:8044-8055(2002). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; 15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
DNA-directed RNA polymerase III subunit 127.6 kDa polypeptide
FCC 2.7.7.6) (RNA polymerase III subunit 2) (RPC2). SEQUENCE FROM N.A. MEDLINE=22278866; PubMed=12391170; Hu P., Wu S., Sun Y., Yuan C.-C., Kobayashi R., Myers M.P., Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate {RNA \ (N) .
SUBUNT: RNA polymerase III consists of about 15 different
subunits. This subunit is the second largest component of RNA

polymerase III. SUBCELLULAR LOCATION: Nuclear

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Q9fgn0 arabidopsis
Q8fil36 plasmodium
Q21492 caenorhabdi
O52373 caldicellul
O8mmk4 dicryosteli
Q8mcx2 pseudomonas
Q9adw6 ehrlichia c
Q8fu72 corynebacte
Q8v3p9 swinepox vi
Q23355 caenorhabdi
O12337 marek's dis
Q9u3g5 caenorhabdi
O12337 marek's dis
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Q8v3p6 caenorhabdi
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Q8v3p6 caenorhabdi
Q8v2p8 escherichia
Q8x2b1 escherichia
Q8x2b1 escherichia
Q8x2b2 escherichia
Q8x2b2 callitrichi
Q8x2b1 sativ
Q9yfks oryza sativ
Q9fgs escherichia
Q8x2b1 escherichia
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Q8x5b6 escherichia
Q8x5b7 escherichia
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Q9TD94 streptococc
Q9TD79 dresponia
Q9Jx73 neisseria m
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Q9Jx89 neisseria m
Q8Z45 acherichia
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Q81SQ4
Q91SQ4
Q479G4
Q479G4
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Q479G6
Q475G6
Q84ZB4
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Q81L36
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Q8YF57;
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Q1-MAR-2002 (TrEMBLrel. 20
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Arsenate reductase.
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Q53384 erreptococ
Q25177 bydra atten
Q8bd3 xanthomonas
Q8p613 xanthomonas
P91125 dunaliella
Q9159 salmonella
Q9159 salmonella
Q97684 clostridium
Q8769 athysia cal
Q8681 arxula aden
Q99681 arxula aden
Q99981 arxula aden
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q8G2R4
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Rosidae;

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ACCOUNTE, FOURTH, 10.8.;

RE Brill L.M., Pieternel V.R.;

T. Legumes seed lectin genese: sequence of Mslec2 from Alfalfa, Alfalfa
and Sweet Clover southern blot analysis, and stable transformation of
RT Alfalfa with antisense-lectin constructs.";

L. Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

BR EMBL; Y16754; CAA6356.1; -.

DR HSSP; P04122; LLOE.

DR InterPro; IPR001220; Lectin legA.

DR Pfam; PP00139; lectin legA; 1.

DR ProDom; PD000671; Lectin legA; 1.

DR ProDom; PD000711; Lectin legA; 1.

DR PROSITE; PS00308; LECTIN LEGUME ALPHA; 1.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago.
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                                                                                                                                Last sequence update)
Last annotation update)
                                             279 AA
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                                                                                                 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 100.
Matches 6; Conservative
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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279
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CHAIN 26 ;
SEQUENCE 279 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                             Lectin precursor.
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SEQUENCE FROM N.A.

STRAIN-16M / ATCC 23456 / Biotype 1;

STRAIN-20200109; PubMed=11756889,

MEDLINE=20020109; PubMed=11756889,

A DelVecchio V.G., Kapatral V., Fatkar R.J., Patra G., Mujer C., Los T.,

La Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman B.,

A Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman B.,

A Haselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

The genome sequence of the facultative intracellular pathogen

E Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

R EMBL, AEOSSOGO2, AALS2881.1;

R Fam., PF01451; LMMPc; 1.

SKART; SMO226; LMMPc; 1.
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MEDLINE. 22247741; PubMed=12271122;

Paulaben I.T., Seehadari R., Nelson K.E., Eisen J.A., Heidelberg J.F., Paulaben I.T., Seehadari R., Durkin A.S., Kolonay J.F., Madupu R.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E., Riedmuller S., Tettelin H., Gill S.W., White O., Salzberg S.L., Indefauller L.L., Lindlar L.B., Halling S.M., Boyle S.M., Fraser C.M.; The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts "; Proc. Natl. Acad. Sci. U.S.A., 99:13148-13153 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Brucella melitensis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBL_TaxID=29461;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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100.0%; Pred. No. 29;
iive 0; Mismatches 0;
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SEQUENCE 157 AA
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                                                                                              NCBI_TaxID=29459;
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SEQUENCE 157 AA.
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MEDLINE=93000998; PubMed=1368792;
Estrada M.P., Hernandez L., Perez A., Rodriguez P., Serrano R.,
Rubiera R., Pedraza A., Padron G., Antuch W., de la Fuente J.,
                                                                                                                                                                                                                                                                                                                                                   "High level expression of streptokinase in Escherichia coli.";
Biotechnology 10:1138-1142(1992).
BMBL: 946536; AACGG418.1; -.
InterPro; IPRO40993: Baphylokinase.
Pfam; PF02821; Staphylokinase; 3.
SEQUENCE 414 AA; 47254 MW; F75BE5831B766904 CRC64;
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                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Created)
Last sequence update)
Last annotation update)
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100.0%; Pred. No. 82;
ative 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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Best Locy Matches

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100.0%; Score 30; DB 16; Length 1041;
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE 1041 A
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Q8P613
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STRAIN=306 / ATCC 13902 / XV 101;
MEDIATRE=22022145; Pubhed=12024217;
MEDIATRE=22022145; Pubhed=12024217;
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Receptor protein-tyrosine kinase (Fragment).
Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
NCBI_TaxID=6087;
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Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Ganthomonadales; Xanthomonadaceae; Xanthomonadaceae; Xanthomonadaceae; Xanthomonas.
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R InterPro: IPR00110; Ig-like.
R InterPro: IPR00110; Ig-like.
R InterPro: IPR001006; Ig-MHC.
R InterPro: IPR001245; Tyr_Dkinase.
R Pfan; PF00047; Ig. 2.
R Pfan; PF00069; Prot Kinase; I.
R PRINTS; PR00109; TYRKINASE.
R PRODOID: PR00109; TYRKINASE.
R PRODOIT: PR00109; IG. Like; I.
R PROSITE; PS00119; PROTEIN KINASE DOM; I.
R PROSITE; PS00119; PROTEIN KINASE DOM; I.
R PROSITE; PS00119; PROTEIN KINASE DOM; I.
R PROSITE; PS00119; PROTEIN KINASE TYR; I.
R ATP-binding; A Kinase; Transferase; Tyrosine-protein kinase.
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STRAIN=UCI;
Chen R.L., Steele R.E.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U24116; AAA65223.1;
HSSP; P11362; 1FGK.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 30; DB 5; L 100.0%; Pred. No. 1.8e+02;
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| 157 SVDVEY 162
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Q8PHD3
AC Q8PHD3;
DT 01-OCT---
DT 01-OCT---
DE ACRIFICATION
GN XANTHOM
CC BACTETION
CC CANTHOM
CC BACTETION
CC CANTHOM
CC BACTETION
CC CANTHOM
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Clearelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Remighieri E.F., Franco M.C., Gregio C.C., Gruber A.,
Ratsuyama A.M., Kishi L.L., Lengelo C.C., Gruber A.M., Lemos M.V.F.,
Locali B.C., Machadnis J.M., Martinez-Rossi N.M.,
Martins E.C., Machadnis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
An Moreira L.M., Novo M.T.M., Omnora V.E., Oliveira M.C., Oliveira V.R.,
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
Spinola L.A.F., Tarkita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
Setubal J.C., Kitajima J.P.,
Tromparison of the genomes of two Xanthomonas pathogens with differing
Nature 417,459-463(2002).
EMBL: AEO11978; AAM38169.1, -
REEL, REO11978; ARELAVINEP.
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REALINE-ATCC 33913 / NCPPB 528;

REALINE-ATCC 33913 / NCPPB 528;

REALINE-2022145; PubMed=1024217;

REALINE-2022145; PubMed=1024217;

REALINE-2022145; PubMed=10.0.4., Reinach F.C., Farah C.S., Furlan L.R.,

Realine C., Cannavan F.C., Cardozo J., Chambergo F., Ciapina L.P.,

Ranacotte G., Cannavan F.C., Cursino-Santog J.R., El-Dorry H.,

Raria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Rormighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

Rormighieri E.C., Machado M.A., Madira A.M.B.N., Martinez-Rossi N.M.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.Y.F.,

Rormighieri E.C., Machado M.A., Madira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Marting E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Marting E.C., Meidanis J., Man, J.D., Silva C., de Soura N.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixaira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Rocmparison of the genomes of two Xanthomonas pathogens with differing the perfective of the genomes of two Xanthomonas pathogens with differing the parameters of two Xanthomonas pathogens with differing the parameters of two Xanthomonas pathogens with differing the comparison of the genomes of two Xanthomonas pathogens with differing the comparison of the comparison of two Xanthomonas pathogens with differing the comparison of the comparison of two Xanthomonas pathogens with differing the comparison of the comparison of two Xanthomonas pathogens with differing the comparison of two Xanthomonas pat
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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EMBL, AE012433, AAM42439.1, ..
InterPro, IPR001036, Acrflvin_res.
Pfam: PF00873, ACR_tran; 1.
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ACRF OR XCC3169.
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Complete proteome.
SEQUENCE 1041 AA; 112760 MM
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Conservative 0
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Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
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O16567
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Dunaliellaceae; Dunaliella.
NCBI_TaxID=3046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 13, Last annotation update)
DE Nicotinic acetylcyoline receptor Dalpha 4 subunit (Fragment)
3N NACR-ALPHA-808 OR NACALPHA-808 OR CG12414 OR CG17552.
C Drosophila melanogaster (Fruit fly)
C Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
C Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
K NCBL TaxID=7227;
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                                        Indels
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Pfam; PF00405; transferrin; 5.
PRINTS; PR00422; TRANSFERIN.
SMART; SM00094; TR FER; 1.
SEQUENCE 1274 AA; 136668 MW; 6C2EE9D914097699 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Fisher M., Gokhman I., Pick U., Zamir A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U77059; AAB36531.1; -.
HSSP; P56410; 1AOV.
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Last annotation update)
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   100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2003 (TrEMBLrel. 23,
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                               1 SVDVEY 6
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P93125
LD P9313
AC P9311
AC P9311
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AC P9311
AC P9312
AC P01
AC P
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STRAIN-CTIB's PLASMID-DHCM1;

MEDLINE=21534947; PubMed=1167608;

MEDLINE=21534947; PubMed=1167608;

A Barkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

A Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

A Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

A Cronin A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

A Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Mitchead S., Barrell B.G.;

RC "Complete genome sequence of a multiple drug resistant Salmonella

R enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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MEDLINE=20280091; PubMed=10773089;
MEDLINE=20280091; PubMed=10773089;
Sherburne C.K., Lawley T.D., Gilmour M.W., Blattner F.R., Burland V., Grotbeck E., Rose D.J., Taylor D.E.;
"The complete DNA sequence and analysis of R27, a large IncHI plasmid from Salmonella typhi that is temperature sensitive for transfer.";
Nucleic Acids Res. 28:2177-2186 (2000).
                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhi.
Plasmid R27, and Plasmid pHCM1.
Pateria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae, Salmonella.
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Pred. No. 23;
   Length 60;
                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
0rf, hypothetical protein (Hypothetical 8.2 kDa protein)
R0092 OR HCM1.13C
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EMBL, AL513383; CAD09627.1; -.
Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 74 AA; 8199 MW; DCC7A8A73B746EAF CRC64;
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Last annotation update)
         'n,
96.7%; Score 29; DB
83.3%; Pred. No. 18;
                                                         1; Mismatches
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Similarity 83.3%;
5; Conservative 1
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Pfam; PF00702; Hydrolase; 1. PRINTS; PR00413; HADHALOGNASE. TIGRPAMs; TIGR01509; HAD-SF-IA-v3; 1.

InterPro; IPR005834; Hydrolase

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Mulson R., Anscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copesy T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopera A., Saunders D., Shownkeen R.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
= 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 5; Length 186;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF016658 166044.1;
WormPep; B00047.4; CE6044.1;
InterPro; IPR002083; MATH.
Pfam; PF00917; MATH; 1.
SMART; SM0061; MATH; 1.
SEQUENCE 186 AA; 21527 MW; 9E216690AB0E1469 CRC64;
                                                                                                                                                                                                                                                                                                                                                        Pauley A., Goela D., Ozersky P.;
"The sequence of C. elegans cosmid B0047.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                             STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
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83.3%;
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                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                      Pauley A., Goela D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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MEDLINE=21359325; PubMed=1146286; MEDLINE=21359325; PubMed=1146286; MeDLINE=21359325; PubMed=1146286; MoDLINE=21359325; PubMed=1146286; MoDLINE=21359325; PubMed=1146286; MoDLINE=21359325; PubMed=16040, V. Modling J., Molf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetoburylicum."; Dateriol. 183:4823-4838(2001).

EMBL, AE007819; AAK81166.1; —
InterPro; IPR005893; HIgnase/hydrlase.
                                                                                                                               Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Predicted phosphatase, HAD superfamily.
                    215 AA
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                                    Q97E84;
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01-MAR-2002 (TEBMBLE-1. 20, Created)
01-MAR-2002 (TEBMBLE-1. 20, Last sequence update)
01-MAR-2003 (TEBMBLE-1. 23, Last annotation update)
01-MAR-2003 (TEBMBLE-1. 23, Last annotation update)
Non-alpha nicotinic acetylcholine receptor subunit.
Aplysia californica (California sea hare).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Heterobranchia; Buthyneura; Opisthobranchia; Anaspidea;
Aplysioidea; Aplysiidae; Aplysia.
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"Non-alpha nicotinic acetylcholine receptor subunit from the
individual identified neurons of Aplysia californica.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori
Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                           Baččeria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Wigglesworthia,
NCBI_TaxID=164609;
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                                                                                                        Query Match 96.7%; Score 29; DB 16; Length 215; Best Local Similarity 83.3%; Pred. No. 71; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.7%; Score 29; DB 16; Length 360; 83.3%; Pred. No. 1.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the endocellular obligate symbiont of
                                                             Complete protecme.
SEQUENCE 215 AA; 24421 MW; C4334F6313CBFC15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 AA; 41359 MW; CA18CB13C1B8492B CRC64;
                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flies, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24654.1; -.
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                               Wigglesworthia brevipalpis.
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Best Local Similarity 83....
S; Conservative
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SIDVEY 30
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Q8CWIS
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                            .crococcineae, Micrococcaceae, Arthrobacter.
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Beet Local Similarity 83.5%,
Then 5; Conservative
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STRAIN=NRRL B-2979;
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                                               NCBI_TaxID=1665;
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Q9FGN0
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Manteuffel R., Stoltenburg R., Kunze G.;
Manteuffel R., Stoltenburg R., Kunze G.;
Manteuffel R., Stoltenburg R., Kunze G.;
Monteuffel R., Stoltenburg R., Kunze G.;

"Post retransport system in budding cells and mycelia of the yeast Arxula adeninivorans LS3.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AU277833; CAB90817.1; -..

InterPro; IPR001117; Cu-oxidase.

InterPro; IPR001117; Cu-oxidase.

InterPro; IPR001117; Cu-oxidase.

InterPro; IPR00194; Cu-oxidase; 3.

PROSITE; PS00009; MULTICOPPER OXIDASE1; 1.
                                                                                                                                                                                                                                                                                                       Gaps
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Saccharomycetales; Dipodascaceae; mitosporic Dipodascaceae; Arxula.
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                  InterPro; IPR006029; Neu_Channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRIMTS; PR00252; NRIONCHĀNNEL.
TIGRNEMA; TIGRO0660; LIC; 1.
PROSITE; PS00236; NEUROTR_ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.7%; Score 29; DB 3; Length 615; 83.3%; Pred. No. 2.2e+02; ative 1; Mismatches 0; Indele
                                                                                                                                                                                                                                                       Length 547
                                                                                                                                                                                                                                                96.7%; Score 29; DB 5; Length 547
83.3%; Pred. No. 1.9e+02;
rative 1; Mismatches 0; Indels
                                                                                                                                                                                                      547 AA; 62535 MW; 3D3F011D78605C91 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ferro-O2-oxidoreductase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN 2001 (TrEMBLrel. 17, Created)
01-JUN 2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
N.N-dimethylglycine oxidase.
DMG.
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  InterPro; IPR006202; Neur_chan_LBD
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18 615 FE
615 AA; 69624 MW;
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Best Local Similarity 83.35,
1.100 5; Conservative
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es 5; Conservative
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155 SIDVEY 160
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                                                                                                                                                                                        Transmembrane
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                                                                                                                                                                                                           SEQUENCE
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Q9AGP8;
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1098661
1009866
DT 01-0C
DT 01-0C
DT 01-1C
DE FETTO
GN AFETTO
OC SECULA
OC SEQUE
RR SEQUE
RR WATTAIL
RA WATTAIL
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Q9AGP
ID Q9AGP
DT 01-UN
DT 01-UN
DD 01-MA
DD NN-G
GN DMG.
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similarity to unknown protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantas, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Meskys R., Harris R.J., Casaite V., Basran J., Scrutton N.S., "Genetic organization of the genes involved in dimethylglycine and sarcosine degradation in Arthrobacter spp.: implications for glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
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PRELIMINARY; PRT; 862 AA.
OBIL36;
O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
PR14 0413.
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 96.7%; Score 29; DB 10; Length 836; Best Local Similarity 83.3%; Pred. No. 3e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       96.7%; Score 29; DB 2; Length 830;
83.3%; Pred. No. 3e+02;
iive 1; Mismatches 0; Indels
                                                                     betaine catabolism.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF329477; AAK16482.1;
                                                                                                                                           Interpro; IPR006222; GCV T.
Interpro; IPR006022; GCV T.
Interpro; IPR00000594; ThiF_domain.
Interpro; IPR000594; ThiF_domain.
Pfam; PP01571; GCV T; 1.
SEQUENCE 830 AA; 89984 MW; 13DE3C4B3DF325DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9FGNO,
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              836 AA
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Q81L36
DD Q81L33
AC Q81L3
DT 01-MA
DT 01-MA
DE HYPOT
GN PF14
GN PF14
CO BUARR
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Length 1154;

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Conservative
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Les 5; Conservative
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117 SVDIEY 122
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       Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                     1 SVDVBY
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OBMMK4:
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                                                                               A Gardner M.J. Hall N. Fung E., White O., Berriman M., Hyman R.W., WA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., WA Gardner M.J., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Barlen J.A., Rutherford K.E., Salzberg S.L., Craig A., Kyes S., A. Ersen J.A., Nene V., Shallom S.J., Suh B., Peterson J. Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vardya A.B., Martin D.M.A., Farlandh A.H., Fraunholz M.J., Roos D.S., Ralph S.A., W. Pertea G.I., Cummings L.M., Subramanian G.M., Mungall C., Pavis R.W., Praser C.M., Barrell B., The Genome sequence of the human malaria parasite Plasmodium at alciparum.", The Construction of the human malaria parasite Plasmodium and Hypothetical procein.

Rembi, Aboliscal Procein.

SEQUENCE 862 AA; 102256 MW, C0073FA8200E178C CRC64;
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N DIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- STMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
BEMEL, U00050; AAA50695.2; -.
WORMPEQ: FO9F7.3, CE30663.
InterPro; IPRO01572; RNA POL BETA; 1.
PROSITE; PS01166; RNA POL BETA; 1.
PROSITE; PS01166; RNA POL BETA; 1.
PROSITE; PS01166; RNA POL BETA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 129.1 kDa protein (EC 2.7.7.6) (DNA-directed RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.7%; Score 29; DB 5; Length 862
83.3%; Pred. No. 3.1e+02;
Live 1; Mismatches 0; Indels
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STRAIN=Bristol N2;
Pauley A.;
The sequence of C. elegans cosmid FOSF7.";
Submitted (MAX-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                   MEDLINE=22255705; PubMed=12368864;
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STRAIN=BRISEOl N2;
MEDLINE=99069613; PubMed=9851916;
Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.5.
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Caenorhabditis elegans.
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[1]
SEQUENCE FROM N.A.
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Q27492;
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027492
AC 027493
AC 027493
DT 01-NO7
DT 01-NO7
DE DE HYDOLI
DE HYDOLI
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OC CACHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Caldicellulosiruptor sp. Rt69B.1.
Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
Caldicellulosiruptor.
NCBI_TaxID=70295;
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL. HYDROLASES).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Rt69B.1;
Morris D.D., Gibbs M.D., Ford M., Thomas J., Bergquist P.L.
"Family 10 and 11 xylanase genes from Caldicellulosiruptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.7%; Score 29; DB 2; Length 1595; 83.3%; Pred. No. 6e+02; ive 1; Mismatches 0; Indels
                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF001018; CBM - 9.1.3.
Pfam; PF001018; CBM - 9.1.3.
Pfam; PF001018; CBM - 9.1.4.
PRINTE; PR001019; GLHYDRLASE10.
SWART; SM00633; Glyco - 10, 1..
PROSITE; PS00593; Glyco - 10, 1..
PROSITE; PS00593; Glyco - 10, 1..
Glycosidase; Hydrolase; Xylan degradation.
SEQUENCE 1595 AA; 178404 MW; BC31B2363F30EF5B CRC64;
                                                                                                                                                                                                                                                                                                                     01.JUN-1998 (TrEMBLrel. 06, Created)
01.JUN-1998 (TrEMBLrel. 06, Last sequence update)
01.MAR-2003 (TrEMBLrel. 23, Last annotation update)
Family 10 xylanase (EC 3.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-Ycogen synthase (EC 2.4.1.21).
Dictyostellum discoideum (Slime mold).
Eukaryott, Mycetcozoa, Dictyostellium.
NGDI_TAXID=44689;
96.7%; Score 29; DB 5; I
83.3%; Pred. No. 4.2e+02;
iive 1; Mismatches 0
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HSSP, P23860, IKGA.
INTERPROJ IPR003305, CBM_CenC.
INTERPROJ IPR0011000, GlyCo_hydro_10.
INTERPRO, IPR0011119; SLH.
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Gaps

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Matches

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RESULT (2008) ON CONTROL OF CONTR

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SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Kawarabayasi Y., Wamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Usec K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoto S.;
"The entire genomic sequence of Corynebacterium efficiens YS-314.";
EMBL, AP002214; BAC16859.1;
Complete proteome.
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MEDLINE=21624277; PubMed=11752168;
Afonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
Kutish G.F., Rock D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                          MEDLINE=21153566; PubMed=11254561;
Obashi N., Rikhika Y., Ubrer A.;
"Analysis of Transcriptionally Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacreria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Corynebacterium.
NCBI_TaxID=152794;
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                                                                                                                                                                                                                                                                                                             93.3%; Score 28; DB 2; Length 148; 66.7%; Pred. No. 83; ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 148 AA; 17570 MW; AF3545DF658F05BB CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                  Infect. Immun. 69:2083-2091(2001).
EMBL; AF078553; AAK28682.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative alcohol dehydrogenase.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium efficiens.
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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23 SIDIEY 28
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SIDIEY 76
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NCBI_TaxID=10276;
STRAIN=Oklahoma;
                                                                                                                                       chaffeensia.";
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Q8FU72
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Q8V3P9
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MEDLINE=21914557; PubMed=11916376;
Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
Bourkaltseva M.V., Sykilinda N.N., Krylov V.N., Volckaert G.;
"The genome of bactriophage phiKZ of Pseudomonas aeruginosa.";
J. Mol. Biol. 317:1-19(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
Bourkaltseva M.V., Sykilinda N.N., Krylov V.V., Volckaert G.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF399011; AAL83091.1; --
InterPro, IPR001596; Pyrophosphatase.
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBI_TaxID=169683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 17.6 kDa protein.
Brilchia canis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                            96.7%; Score 29; DB 5; Length 2473; 83.3%; Pred. No. 9.5e+02; cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Match 93.3%; Score 28; DB 9; Length 146; Local Similarity 66.7%; Pred. No. 81; les 4; Conservative 2; Mismatches 0; Indels
EMBL; AC117082; AAM34363.1; -.
SEQUENCE 2473 AA; 274970 MW; 6395FD78E45A7945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PS00387, PPASE, Î. SEQUENCE 146 AA; 17037 MW; A1584AF76C9EAC13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     146 AA
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[2]
SEQUENCE FROM N.A.
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STRAIN-OKlahoma;
MEDLINE-98371112; PubMed=9705412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                             Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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SVDIEY 1004
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94 SIDIEY 99
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                                                                                                                                                                                                                                                     666
                                                                                  Query Match
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RESULT 23
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AC 09ADW
DT 01-JU
DT 01-JU
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SORRERES

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SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2001 (TrEMBLrel. 18,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                         Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
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150 SIDIEY 155
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           1 SVDVEY 6
                                 ZC504.2 protein.
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                     RESULT 27
Q9U3Q5
ID Q9U3Q5
AC Q9U3Q5;
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SEQUENCE 136 AA; 15535 MW; D6B9F39529DD5D3A CRC64;

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SEQUENCE FROM N.A.
MEDLINE=97128994; PubMed=8973534;
MEDLINE=97128994; PubMed=8973534;
Jang H.K., Ono M., Kato Y., Tohya Y., Niikura M., Mikami T.;
"Identification of a potential Marek's disease virus serotype 2
glycoprotein D gene with homology to herpes simplex virus glycoprotein
                                                                                                                                                                               Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MormPep (1972) 1191.

MormPep (1972) 1261.

InterPro; IPR006254; Isocit_lyase.

InterPro; IPR00918; Isocit_lyase.

InterPro; IPR00918; Isocit_lyase.ph.

InterPro; IPR001465; Malate_synthase.

Pfam; PF00443; ICL; 1.

Pfam; PF00443; ICL; 1.

ProDom; PF0174; Malate_synthase.ph; 1.

ITGRFAMS; TIGR01346; isocit_lyase.ph; 1.

TIGRFAMS; TIGR01346; malate_syn_A; 1.

PROSITE; PS00161; ISOCITEATE LYASE; 1.

SEQUENCE 907 AA; 101848 MM; AAF64B820B82DIB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.3%; Score 28; DB 5; Length 907; 66.7%; Pred. No. 5.7e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                Matthews L.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Marek's disease-like viruses.
NCBI_TaxID=36353;
   Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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EMBL, 583367, AAB50855.1;
InterPro. 1PR000719; Prot. Kinase.
Pfam, PP00069; pkinase, 1.
ProDom, PD000001; Prot Kinase, 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
ATC. Linding; Kinase; Transferase.
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01-JUL-1997 (TrEMBLrel. 04, Last sequen
01-MAR-2003 (TrEMBLrel. 23, Last annot:
Protein kinase like-protein (Fragment)
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
EMBL; 28316; CAB62784.1; --
HSSP; O53752; IF61.
   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                       Caenorhabditis elegans
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|:||
18 SIDIEY 23
                                                                                             C08F11.14 protein.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                               NCBI_TaxID=6239;
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Science 282:2012-2018(1998).

1. Science 282:2012-2018(1998).

1. Science 282:2012-2018(1998).

1. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

R BMEL; Z50029; CA990341.2; ---

R MOTIMPEP, ZC5042, CC283181.

R InterPro; IPR006201; Neur_chan_LBD.

R InterPro; IPR006202; Neur_chan_LBD.

R InterPro; IPR006202; Neur_chan_LBD.

R Pfam; PF02931; Neur_chan_memb. 1.

R Pfam; PF02931; Neur_chan_memb. 1.

R Pfam; PF02932; Neur_chan_memb; 1.

R Pfam; PF02932; Neur_chan_memb; 1.

R PRINTS; PR00025; NEUROTRAINBEL; 1.

R PROSITE: PS00236; NEUROTRAINBEL; 1.

R PCOSTOCICEIN; Ionic channel; Posteynaptic membrane; Transmembrane.
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                            STRAIN=17077-99;
Afonso C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,
Kutish G.F., Rock D.L.; to the EMBL/GenBank/DDBJ databases.
EMBL, AF410153; AAL69784.1; --
InterPro; IPR004970; Peptidase C57.
Pfam; PF03290; Peptidase C57.
SEQUENCE 433 AA, 51052 MW; 2F9F7F0CB436A7D8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.3%; Score 28; DB 5; Length 579; 66.7%; Pred. No. 3.5e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kershaw J.K.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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"The genome of swinepox virus.";
J. Virol. 76:783-790(2002).
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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388 SIDIEY 393
                                                                                    SEQUENCE FROM N.A.
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Escherichia coli 0157:H7.
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Best Local Similarity 83.3
Matches 5; Conservative
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Q8X2B1;
                                                                                                                                         Kinase.
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SYNERRY
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                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thymidine kinase.
Spodoptera frugiperda ascovirus 1.
Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.
                  90.0%; Score 27; DB 12; Length 136; 83.3%; Pred. No. 1.3e+02; ive 1; Mismatches 0; Indels
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EMBL; U28971; AAA68377.1;
Wormepp; B0244.9; CE01756.
InterPro; IRR01865; Ribosomal S2.
PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of C. elegans cosmid B0244.";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. - SEQUENCE 180 Aa; 20592 MW; 9B41BA9212622FD4 CRC64;
                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 20.6 kDa protein.
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                  Query Match 90.0
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 83.3
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                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.; "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Favello A.;
                                                                                                                                                    92 SMDVEY 97
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                                                                                                            1 SVDVEY 6
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STRAIN=a;
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009968
AC 00996
DT 01-NO
DT 0
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10 08JJY6
10 08JJY
AC 08JJY
DT 01-0C
DT 01-NM
DE Thymi
DE Thymi
OX NCBI
RN [1]
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RR SEQUE
RC STRAIE
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Oryza sativa (japonica cultivar-group).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee Y., Kende H., "Expression of alpha-Expansin and Expansin-Like Genes in Deepwater Rice.";
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SEQUENCE FROM N.A.

MEDLINE=21074913, PubMed=11206551,

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gammaproteobacteria; Enterobacteriales,
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U-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last amontation update)
Putative tail fiber protein encoded within prophage CP-933V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 27; DB 10; Length 213; 83.3%; Pred. No. 2.1e+02; ive 1; Mismatches 0; Indels
Stasiak K., Renault S., Demattei M.V., Bigot Y., Federici "Evolution of Ascoviruses from Iridoviruses"; submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AJ312699, CAC84464.1; -. InterPro; IPR002624; dNK.
                                                                                                                                                                                                            Query Match 90.0%; Score 27; DB 12; Length 21 Best Local Similarity 83.3%; Pred. No. 2.1e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                   SEQUENCE 210 AA; 24522 MW; 9B28484AF10C6B79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER 1 1 1
SEQUENCE 213 AA; 23205 MW; F2AB23F4B257C70B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Physiol. 130:1396-1405(2002).
EMBL; AY100693; AAM52409.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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MEDLINE=22315554; PubMed=12428004;
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Enterobacteriaceae, Escherichia
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Gaps

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RY RY SO KW SO KW

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MEDLINE=20479972; PubMed=11029001; Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
"Oryza sativa chromosome 10 BAC OSJNBb0015111 genomic sequence."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 275;
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Thermoplasmataceae, Thermoplasma.
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                                                                                                                                                                                      InterPro; IRR007112; Expan_endogl.
InterPro; IRR007111; Expan_Lol_pl.
InterPro; IRR007111; Expan_Lol_pl.
InterPro; IRR007117; Expan_Lol_pl.
Pfan; PF01157; Pollen allergen; 1.
PRODITS; PR0125; EXPANSNFAMLY.
PRODITE; PS50843; EXPANSIN_CRD, 1.
PROSITE; PS50842; EXPANSIN_E045; 1.
SEQUENCE 275 AA; 29301 NW; E088C7DF05596AIC7 CRC64;
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EMBL; AL445064; CAC11632.1; -.

Interpro; IPR02035; VWF.A.

SYMARY; SM00327; VWA; 1.

SEQUENCE 277 AA; 31081 WW; 7DB9492F1A735CD6 CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Ta0490.
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Last sequence update)
Last annotation update)
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83.3%; Pred. No. 2.8e+02;
iive 1; Mismatches 0;
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Pred. No. 2.8e+02;
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01-0CT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
Expansin-like protein 1.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 AVDVEY 146
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Best Local Similarity
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                                                                                                                                                               Gramene; Q9FWF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2303;
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Matches
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081GS6
1D 081GS8
AC 081GS
DT 01-0C
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STRAIN-O157.HT / RIMD 0509952;

MEDLINE-21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Kuhara M., Maka M., Maka
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Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.B.,
Bowman C.L., Crauven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
               Welch R.A., Blattner F.R.; Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Meture 409:529-533(2001).
BMBL; AE005440; AAG57198.1; -.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Elrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                              Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.0%; Score 27; DB 16; Length 271; 83.3%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                    90.0%; Score 27; DB 16; Length 277
83.3%; Pred. No. 2.76+02;
Minmarches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                            Complete proteome.
SEQUENCE 271 AA, 27706 MW; CE4D5CB197B83B1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative tail fiber protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative pollen allergen.
OSJNBB0015111.10.
                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
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SMDVEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 SMDVEY 57
                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
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Q8X298;
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108829
AC 08829
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AC 08829
DT 01-MADT 01-MADT
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109FWF
AC Q9FWF
AC Q9FWF
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
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GN OCYZAG
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MEDINE_21107697; PubMed=11158621;
MEDINE_21107697; PubMed=11158621;
MEDINE_21107697; PubMed=11158621;
MAID F.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.0%; Score 27; DB 17; Length 307; 83.3%; Pred. No. 3.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.0%; Score 27; DB 12; Length 302; Best Local Similarity 83.3%; Pred. No. 3.1e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrobaculum aerophilum,
Archaea; Crenarchaecta; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 AA; 33783 MW; 07134831A775D358 CRC64;
                                                                                                                                                                                                                                                                                           Viruses, dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
NCBI_TaxID=106331;
                                01-JUN-2001 (TrBMBLrel. 17, Created)
01-JUN-2001 (TrBMBLrel. 17, Last sequence update)
01-OCT-2001 (TrBMBLrel. 18, Last annotation update)
ORF54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
REMBL, AE09924; AALG4835.1; -.
RINterPro; IPR006139; 2-Hacid_DH.
R Pfam; PF00389; 2-Hacid_DH. DH.
R Pfam; PF00389; 2-Hacid_DH. 1.
R Pfam; PF00389; 2-Hacid_DH. 1.
R PROSITE; PS00670; D_2 HYDROXYACID_DH_2; 1.
R PROSITE; PS00671; D_2 HYDROXYACID_DH_3; 1.
302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AA
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
PubMed=11792869;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                         Callitrichine herpesvirus 3.
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Best Local Similarity 83.5-
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||||
221 AVDVEY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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76 NVDVEY 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8ZTC7
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.0%; Score 27; DB 10; Length 279; 83.3%; Pred. No. 2.8e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                            "Expression of expansin-like genes in rice internodes."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. -- I- SINILARITY: BELONGS TO THE EXPANSIN FAMILY. EMBL, AXO3902A AXO34681.1; -- Gramene; Q8LGS6; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gramene; OBLSG4; -.
InterPro; IPR007112; Expan_endogl.
InterPro; IPR007112; Expan_endogl.
InterPro; IPR007118; Expan_Lol_pi.
InterPro; IPR007117; Expan_Lol_pi.
Pfam, PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
PROSITE; PS50843; EXPANSIN_ED_pi. C; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
SEQUENCE 289 AA; 31238 WW; 5EF4D782ATEF7322 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; JPR00112; Expan_endogl.
InterPro; JPR001118; Expan_Lol_pl.
InterPro; IPR007118; Expan_Lol_pl.
InterPro; IPR007118; Expan_Lol_pl.
Pfam; PF01235; Pollen allergen; 1.
PRINTS; PR01225; EXPANSNAMLY.
PRODOM; PD002179; EXPANSIN CBP; 1.
PROSITE; PS50843; EXPANSIN CBP; 1.
SEQUENCE 279 AA; 30038 MW; FD9B86ASA6A9BA2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 A.A.
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Oryza sativa (japonica cultivar-group).
Ehrhartoideae, Oryzeae, Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3,
"-hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | | | | | | 146 AVDVEY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||||
146 AVDVEY 151
                                                                                                                                           SEQUENCE FROM N.A.
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MEDLINE=96239055; PubMed=8675344;
Shang E.S., Summers T.A., Haake D.A.;
"Molecular cloning and sequence analysis of the gene encoding LipL41,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitebh E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
VCBI_TaxID=173;
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NCBI_TaxID=29507;
                                                                                                                                                                                     "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141.147(202).
EMBL; AL93113; CA52172.1; -.
Interpro; IPR002491; Peripla_BP.
Pfam; PF01497; Peripla_BP_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 349;
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83.3%; Pred. No. 3.6e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       349 AA; 36642 MW; 2E3B2A72B6BF780A CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morris K.K.;
Thesis (1995), University of California, Davis.
EMBL; U31426; AAB09404.1; -.
Lipoprotein.
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Best Local Similarity 83.5.
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LIPL41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team,
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMEL, AKO89832; BAC39034.1; -.
SEQUENCE 320 AA; 34522 MW; 91DC3FBP778631C8 CRC64;
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STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.0%; Score 27; DB 11; Length 320; Best Local Similarity 83.3%; Pred. No. 3.3e+02; Matches 5; Conservative 1; Mismatches 0; Indels
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
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NCBI TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
MEDLINE=22354683; PubMed=12466851;
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Ceroid-lipofuscinosis. Mus musculus (Mouse).
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                   23,
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                                                                                                           PRELIMINARY;
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STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpides N., Overbeek R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
J. Bacteriol, 184:2005-2018 (2002).
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    Fusobacterium nucleatum strains and a model for the topology of the
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                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 27; DB 2; Length 368; 83.3%; Pred. No. 3.88+02; Artive 1; Mismatches 0; Indels
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Bacteria; fusobacteria; fusobacterales; fusobacteriaceae;
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
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CHAIN 21 368 PORIN.
SEQUENCE 368 AA, 42373 MW; 3B20A95BBE66D23C CRC64;
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SEQUENCE 368 AA, 42373 MW; 131624D9EB017626 CRC64;
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01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Major outer membrane protein.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Porin precursor.
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83.3%; Pred. No. 3.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368
                                                 proteins.";
Mol. Gen. Genet. 244:104-110(1994).
EMBL, X72582; CAA51172.1; -.
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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STRAIN=ATCC 10953;
MEDLINE=94316187; PubMed=8041356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 184:2005-2018(200
EMBL; AE010488; AAL93958.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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59 SVDVQY 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusobacterium.
NCBI_TaxID=76856;
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Q47905;
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Q47905
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            RATE SET TES
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MEDLINE=94010332; PubNed=8406032;
MEDLINE=94010332; PubNed=8406032;
Bolstad A.I., Jensen H.B.;
"Complete sequence of only, the structural gene encoding the 40-kDa outer membrane protein of Fusobacterium nucleatum strain Fev1.";
Gene 132:107-112(1993).
Signal.
a surface-exposed lipoprotein of pathogenic Leptospira species.";
Infect. Immun. 64:2322-2330(1996).
EMBL; L46794; AAB06799.1; -.
Interpro, IPR001440; TPR.
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STRAIN-ATCC 25586;
MEDLINE=94316187; PubMed=8041356;
BOlstad A.I., Tommassen J., Jensen H.B.;
"Sequence variability of the 40-kDa outer membrane proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 90.0%; Score 27; DB 2; Length 368; Local Similarity 83.3%; Pred. No. 3.8e+02; es 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        Length 355;
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NCBI_TaxID=851;

        SIĞNAL
        1
        20
        POTENTIAL.

        CHAIN
        21
        368
        OUTER MEMBRANE PROTEIN (40K).

        SEQUENCE
        368
        Aa; 41918
        MW; 13E15C1E2E3DEE82
        CRC64;

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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                        1 19 POTENTIAL.
20 355 POTENTIAL.
355 AA, 38910 MW, 89D2EA08D271DC78 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Outer membrane protein (40K) precursor.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UND-2002 (TrEMBLrel. 21, Last annotation update)
Porin precursor.
                                                                                                                                                                                                                                                                                                                                                                90.0%; Score 27; DB 2; I
83.3%; Pred. No. 3.6e+02;
tive 1; Mismatches 0;
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Best Local Similarity 83.3
Matches 5, Conservative
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23 TVDVEY 28
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59 SVDVQY 64
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                                                                                                                                                                                                                                                     CHAIN
SEQUENCE
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1047903
10 047903
10 04790
11 04790
11 01-NO
11 01-NO
11 01-NO
12 01-NO
13 01-NO
14 01-NO
15 01-NO
16 01-NO
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10 047904
10 04790
AC 04790
DT 01-NO
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Matches
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STRIN=O157:H7 / EDL933 / ATCC 700927;

STRIN=O157:H7 / EDL933 / ATCC 700927;

MEDLINE=210104915; PubMed=11206551;

A REDLINE=210104915; PubMed=11206551;

A Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

B Posfâd G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

A Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

A Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner P.R.;

T "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";

EMBL; AE005290; AAG55515.1; -.

R InterPro; IPR000087; Collagen.

R Pfam; PF01391; Collagen; 2.

Complete proteome.

W Complete proteome.
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                                                                                                                                                                                    Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
WCBL_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bscherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=83334;
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STRAIN=56601 / Serogroup Icterchaemorrhagiae / Serovar lai;
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90.0%; Score 27; DB 16; Length 37
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                    Ren S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE011248; AAN47815.1;
Lipoprotein; Complete proteome.
SEQUENCE 374 AA; 41070 MW; 3A3F9EB94BFDCIAO CRC64;
                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane lipoprotein lipL41.
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Best Local Similarity 83.3
Matches 5, Conservative
                                                                   PRELIMINARY;
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42 TVDVEY 47
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                                                                Q8F8E1
Q8F8E1;
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                                RESULT 49
Q8F8E1
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MEDLINE=96179239; PubMed=8596665;
Bolstad A.I., Hogh B.T., Jensen H.B.;
"Molecular characterization of a 40-kDa outer membrane protein, FomA, of Fusobacterium periodonticum and comparison with Fusobacterium nucleatum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oral Microbiol. Immunol. 10:257-264(1995).
EMBL. X82023, CAA5747.1; -. MAJOR OUTER MEMBRANE 40KDA PROTEIN FOMA.
SEQUENCE 372 AA; 42265 WM; 5DFC806A50D48F56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Bolstad A.I., Tommassen J., Jensen H.B.; "Sequence variability of the 40-kDa outer membrane proteins of Fusobacterium nucleatum strains and a model for the topology of the
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90.0%; Score 27; DB 2; Length 372;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                    Bolstad A.I.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 10953;
Jensen H.B.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                    Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                    Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
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CHAIN 21 370 PORIN.
SEQUENCE 370 AA; 42241 MW; 781611E6F206012F CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Major outer membrane 40KDa protein FomA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 372 AA.
                                                       proteins.";
Wol. Gen. Genet. 244:104-110(1994)
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Matches 5, Conservative
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                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 10953;
Bolstad A.I.;
                                                                                                                  STRAIN=ATCC 10953;
Bolstad A.I.;
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59 SVDVQY 64
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SIGNAL
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Search completed: January 20, 2004, 13:57:40 Job time : 39 secs

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Sequence 5954, PAS Sequence 62, Appl Sequence 61, Appl Sequence 114, Appl Sequence 54666, A Sequence 1285, Ap Sequence 15897, Ap
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Sequence 25695, A
Sequence 26860, A
Sequence 3243, Ap
Sequence 11, Appl
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Sequence 15897, A
Sequence 3474, Ap
Sequence 7251, Ap
Sequence 7251, Ap
Sequence 692, App
Sequence 43, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Appl
Sequence 36165, A
Sequence 6610, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                     Description
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1. /cgn2 6/ptodata/1/paa/USO6_NEW COMB.pep:*

2. /cgn2 6/ptodata/1/paa/USO6_NEW COMB.pep:*

3. /cgn2 6/ptodata/1/paa/USO8 NEW COMB.pep:*

3. /cgn2 6/ptodata/1/paa/USO9 NEW COMB.pep:*

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3. /cgn2 6/ptodata/1/paa/USO0 NEW COMB.pep:*

3. /cgn2 6/ptodata/1/paa/USO0 NEW COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                         354356 segs, 73659510 residues
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Maximum Match 100%
Listing first 75 summaries
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Maximum DB seq length: 200000000
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5-10-425-114A-400 5-10-425-114A-640 5-10-415-182A-9891 5-10-415-182A-9891 5-10-415-182A-691 5-10-473-040-683 5-10-473-90-5786	S-10-679-063-16 S-10-679-063-21 S-10-679-063-21 S-10-679-063-27 S-10-451-168-56 S-10-451-168-57 S-09-614-150A-1 S-09-614-150A-3 S-10-418-8618-4	5.10 - 478 - 881 B - 5.10 - 478 - 881 B - 5.09 - 581 - 286 A - 5.09 - 581 - 286 A - 5.09 - 581 - 586 A - 5.09 - 581 -	1472-1444.3 / 128 1472-260-1160.2 / 125-1164.4 / 125-1164.4 / 146.3 / 125-1164.4 / 146.3 / 125-1164.5 / 126.3
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## ALIGNMENTS

RESULT 1
US-10-415-182A-829B
is Sequence 8298, Application US/10415182A
is GENERAL INFORMATION:
i APPLICANT: Telford, John
if TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
i FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/415,182A
i CURRENT FILING DATE: 2000-12-09
i PRIOR PAPLICATION NUMBER: GB-0026333.5
PRIOR APPLICATION NUMBER: GB-002672.6
i PRIOR APPLICATION NUMBER: GB-0105640.7
i PRIOR APPLICATION NUMBER: GB-0105640.7
i PRIOR APPLICATION NUMBER: GB-1005640.7
i NUMBER OF SEQ ID NOS: 12024
i SEQ ID NO 8228
i SEQ ID NO 8228
i LENGTH: 440

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APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Friedrich, Thomas
APPLICANT: Elemerman, Norbert
APPLICANT: Sturmer, Rainer.
TITLE OF INVENTION: Galyan oxidase and of a reducing agent
FILER REFERENCE: BGI-156US
CURRENT APPLICATION NUMBER: US/10/474,601
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: PCT/EP02/03873
PRIOR PILING DATE: 2003-10-09
PRIOR PILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.7%; Score 29; DB 5; Length 1190; 83.3%; Pred. No. 1.5e+03; ive 1; Mismatches 0; Indel8
                                                                                      Score 29, DB 6; Length 615;
Pred. No. 1.2e+03;
1; Mismatches 0; Indels
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CURRENT PELING DATE: 2000-07-11

PRIOR PELING DATE: 2000-07-11

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: 60/173,93

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: 60/156,93

PRIOR FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: 60/194,831

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-27

NUMBER OF SEQ ID NOS: 43008

SEQ ID NOS: 43008

SEQ ID NOS: 43008

SEQ ID NOS: 43008
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; Sequence 3243, Application US/09614150A
; GENERAL INFORMATION:
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; ORGANISM: Arxula adeninivorans US-10-679-063-26860
                                                                                             96.7%;
83.3%;
                                                           APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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ORGANISM: DROSOPHILA
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APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRENT APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/191,637

PRIOR APPLICATION NUMBER: 60/191,647
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GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
ITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15.52054) B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 26860
LENGTH: 615
TYPE: PRT
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Pred. No. 1.1e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 25695, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-415-182A-8298
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83.3%;
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 83.3
Matches 5, Conservative
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ORGANISM: DROSOPHILA
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US-09-614-150A-25695
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| US-GU-WB3-J-1/-bb|
| Sequence 60, Application US/60483917 |
| GENERAL INFORMATION: | Application US/60483917 |
| GENERAL INFORMATION: | Application US/60483917 |
| APPLICANT: Gan, Li
| APPLICANT: Chin, Daniel J
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APPLICANT: Gan, Li
APPLICANT: Chin, David
APPLICANT: Chin, David
APPLICANT: Chin, David
APPLICANT: Chin, David
APPLICANT: Organize Juliant
TITLE OF INVENTION: NUCLEIC ACIDS ASSOCIATED WITH NEURODEGENERATIVE DISORDERS
FILE REFERENCE: 00208.0013.PZUS00
CURRENT FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 562
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Pred. No. 2.1e+03;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 90.0%; Score 27; DB 5; 183.3%; Pred. No. 2.1e+03; ive 1; Mismatches 0;
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25556
LENGTH: 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 62, Application US/60483917; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT CAGANISM: Rattus norvegicus US-60-483-917-60
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Mus musculus
US-60-483-917-62
                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: DROSOPHILA
US-09-614-150A-25056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 SVDMEY 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 SLDVEY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SVDVEY 6
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US-60-483-917-62
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Coul, Yihua
APPLICANT: Coul, Yihua
APPLICANT: Coul, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Coul, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 194-28
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 59564
LENGTH: 268
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/09/614,150A
CURRENT APPLICATION NUMBER: US/09/614,150A
CURRENT FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PELING DATE: 1999-10-28
PRIOR PELING DATE: 1999-10-28
PRIOR PELING DATE: 1999-11-28
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PELING DATE: 1999-11-28
PRIOR APPLICATION NUMBER: 60/175,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                          90.0%; Score 27; DB 6; Length 17; 83.3%; Pred. No. 6.3e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Clone ID: LIB3587-216-D2_FLI.pep
US-10-425-114A-59564
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US-09-614-150A-25056
; Sequence 25056, Application US/09614150A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 59564, Application US/10425114A; GENERAL INFORMATION:
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Matches 5, Conservative
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Matches 5, Conservative
       ; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
: ORGANISM: Pichia pastoris
US-10-474-601-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | | | | | | 68 TVDVEY 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
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1 NVDVEY 6
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US-10-425-114A-59564
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Gaps
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i Sequence 25025, Application US/10679063

j GENERAL INFORMATION: Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

PILE REFERENCE: 38-15(52054)B

CURRENT APPLICATION NUMBER: 60/415,758

PRIOR PELING DATE: 2003-10-02

PRIOR PELING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 27373

SEQ ID NO 25025

LENGTH: 160

TYPE: PRI
CORGANISM: Glycine max

US-10-679-063-25025
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TITLE OF INVENTION: TRANGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 30-15 (52054)B
CURRENT APPLICATION NUMBER: 0.0010/0.02
PRIOR PILLING DATE: 2003-10-02
PRIOR PILLING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 1285
LENGTH: 164
TYPE: PRI
ORGANISM: Glycine max
               Sequence 1932, Application US/10679063
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR PILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.7%; Score 26; DB 6; Length 158; 83.3%; Pred. No. 1.8e+03; rive 0; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 6; Length 160;
Pred. No. 1.8e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
| NAME/KEY: unaure
| LOCATION: (1)..(158)
| OTHER INFORMATION: unsure at all Xaa locations
| US-10-679-063-1932
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GENERAL INFORMATION:
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Beet Local Similarity 83.33,
Tinhes 5, Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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      US-10-679-063-1932
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US-10-679-063-1285
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Abou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: ADABLEA, Jack E
APPLICANT: Cao, Yongwein
ITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 30-1 (53313) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54666
LENGTH: 140
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Sequence 14, Application US/60482992

Sequence 14, Application US/60482992

GENERAL INFORMATION:

APPLICANT: Li, Weihua

APPLICANT: Reed, Danielle

APPLICANT: Bachmanov, Alexander

                                                                     Gaps
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   90.0%; Score 27; DB 7; Length 563; 83.3%; Pred. No. 2.1e+03; tive 1; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels
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Pred. No. 2.5e+03;
1; Mismatches 0; Indels
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US-10-425-114A-54666
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83.3%;
                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:||||
274 SLDVEY 279
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Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                              1 SVDVEY 6
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ORGANISM: Zea mays
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US-10-425-114A-54666
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CURRENT APPLICATION NUMBER: US/10/415,182A
CURRENT PILING DATE: 2003-12-09
PRIOR PELING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: GB-002872.6
PRIOR APPLICATION NUMBER: GB-015640.7
PRIOR APPLICATION NUMBER: GB-015640.7
PRIOR APPLICATION NUMBER: GB-015640.7
PRIOR FILING DATE: 2001-03-07
NUMBER: SEQ ID NOS: 12024
SEQ ID NO 3474
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GENERAL INPORMATION:
APPLICANT: Roemer, Terry
APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT CANDIDA Albicans PCT-US03-40618-7251
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-741-849-7251
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GENERAL INFORMATION:
APPLICANT: Edgetton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15[2054]B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
SEQ ID NO 25896
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18897. Application US/10679063

GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TILE OF INVENTION: TANGEENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT PILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 18897
                                                                                                              86.7%; Score 26; DB 6; Length 164; 83.3%; Pred. No. 1.9e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 6; Length 164;
Pred. No. 1.9e+03;
0; Mismatches 1; Indels
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Pred. No. 1.9e+03;
0; Mismatches 1;
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(164)
; OTH:R INFORMATION: unsure at all Xaa locations
US-10-679-063-1285
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, Sequence 3474, Application US/10415182A
, GENERAL INFORMATION:
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US-10-679-063-15897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%;
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ilarity 83.3%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Catharanthus roseus
US-10-679-063-25896
                                                                                                                Query Match 86.7
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                               1 SVDVEY 6
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                                                                                                                                                                                                                                                                                              RESULT 15
US-10-679-063-25896
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US-10-679-063-15897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM:
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APPLICANT: Elitra Pharmaceuticals, Inc.
APPLICANT: Elitra Pharmaceuticals, Inc.
APPLICANT: Elitra Canada Limited
TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
CURRENT APPLICATION NUMBER: PCT/US03/40618
CURRENT APPLICATION NUMBER: PCT/US03/40618
CURRENT FILMS DATE: 2003-12-19
FRIOR FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Use
FILE REFERENCE: 10182-023-999
CURRENT APPLICATION NUMBER: US/10/741,849
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 60/434,832
PRIOR FILING DATE: 2002-12-19
APPLICANT: Telford, John
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A &
PILE REFERENCE:
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APPLICANT: Spaceria Acetal A.
APPLICANT: Shimkets Richard A.
APPLICANT: Spice A.
FILE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same CURRENT APPLICATION NUMBER: US/10/701,283
CURRENT FILING DATE: 2003-11-03
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-27
PRIOR PAPLICATION NUMBER: 60/173,165
PRIOR PLING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,544
PRIOR PLING DATE: 1999-12-29
PRIOR PLING DATE: 1999-12-29
PRIOR PLING DATE: 2000-01-04
PRIOR FILING DATE: 2000-01-04
PRIOR FILING DATE: 2000-01-04
PRIOR FILING DATE: 2000-01-04
PRIOR FILING DATE: 2000-01-04
PRIOR PLING DATE: 2000-01-04
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APPLICANT: Special, Steven K
APPLICANT: Spinkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Muralidhara, Padigaru
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Spytek, Spott A.
APPLICANT: Spytek, Spytek, Spott A.
APPLICANT: Spytek, Spott A.
APPLICANT: Spytek, Spytek, Spott A.
APPLICANT: Spytek, Spy
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LOCATION: (1)...(282)
OTHER INFORMATION: Where X is a residue at which the query and
OTHER INFORMATION: Subject seugnces are not identical.
US-10-701-283-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.7%; Score 26; DB 6; Length 282; 66.7%; Pred. No. 2.2e+03; ive 2; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus Sequence
                                                                                                                                                           RESULT 22
US-10-701-283-43
i Sequence 43, Application US/10701283
; GENERAL INFORMATION:
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US-10-701-283-42
'Sequence 42, Application US/10701283
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Spaderna, Steven K APPLICANT: Quinn, Kerry E.
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Best Local Similarity 66...
4; Conservative
215 SADVRY 220
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2 AVDIEY 7
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TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLOO1480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT APPLICATION NUMBER: US/60/495,114
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: PARISEQ for Windows Version 4.0
SEQ ID NO 1576
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Pred. No. 2e+03;
0; Mismatches 0; Indels
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83.3%; Pred. No. 2e+03;
tive 1; Mismatches 0; Indels
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Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels
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| GENERAL INFORMATION:
| APPLICANT: GREENBERG | E. Peter |
| APPLICANT: GREENBERG | E. Peter |
| APPLICANT: SCHENBERG | Martin |
| APPLICANT: CLOSTROH, Candi |
| TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA |
| FILE REFERENCE: UIZ-038CP |
| CURRENT APPLICATION NUMBER: US/10/389,647 |
| CURRENT PEPLICATION NUMBER: 09/653730 |
| PRIOR FILING DATE: 2003-03-14 |
| PRIOR FILING DATE: 1999-09-01 |
| PRIOR FILING DATE: 1999-09-03 |
| NUMBER OF SEQ ID NOS: 710 |
| SOFTHARE: PESESEQ for Windows Version 4.0 |
| LENGTH: 244
                                                                                                                                                                                                                                                                                         86.7%; Scc...
100.0%; Pred. No. ...
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; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-692
                             SOFTWARE: Parentin Version 3.2

SEQ 1D NO 7251

LENGTH: 201

TYPE: PRT

ORGANIEM: Candida albicans

US-10-741-849-7251
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
NUMBER OF SEQ ID NOS: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-60-495-114-1576
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|39 SVEVEY 144
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192 VDVEY 196
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US-10-389-647-692
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3 AVDIEY 8

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GENERAL INFORMATION:

APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: Set al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/09/614,150A
CURRENT FILING DATE: 1999-10-7-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-2-8
PRIOR APPLICATION NUMBER: 60/13,383
PRIOR APPLICATION NUMBER: 60/13,383
PRIOR APPLICATION NUMBER: 60/13,383
PRIOR FILING DATE: 1999-11-2-8
PRIOR APPLICATION NUMBER: 60/13,383
PRIOR APPLICATION NUMBER: 60/13,383
PRIOR APPLICATION NUMBER: 60/13,383
PRIOR FILING DATE: 2000-01-2-8
PRIOR FILING DATE: 2000-01-2-8
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30165
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GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Orbin, Barry S.
APPLICANT: Heaing, Joseph B.
APPLICANT: Heaing, Joseph B.
APPLICANT: Heaing, Joseph B.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Siter, Steven C.
APPLICANT: Spiritdonov, Sergei
TILLO PINVENTYON: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21 (51847)B
CURRENT PPLICATION NUMBER: US/09/897,516A
CURRENT PLLING DATE: 2000-06-30
PRIOR PLICATION NUMBER: US 60/215,161
PRIOR PLICATION NUMBER: US 60/215,161
PRIOR PLICATION NUMBER: US 60/215,161

PRIOR APPLICATION NUMBER: US 60/215,161

SEQ ID NOS: 8415

LENGTH: 316
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                                                                                                                                                                                              Application US/09614150A
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Xenorhabdus sp.
US-09-897-516A-6610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 VDVEY 266
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Sequence 12, Application US/10701283

Sequence 12, Application US/10701283

GENERAL INFORMATION:

APPLICANT: Spacerna, Steven K
APPLICANT: Quinn, Kerry E.

APPLICANT: Muralidhara, Padigaru
APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REPERENCE: 1596-6-60 CIP
FILE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: US/10/701,283

CURRENT APPLICATION NUMBER: US/09/737,149

PRIOR FILING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: 60/173,165

PRIOR FILING DATE: 1999-12-27

PRIOR PLING DATE: 1999-12-27

PRIOR PLING DATE: 1999-12-27

PRIOR FILING DATE: 2000-01-04

PRIOR FILING 
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86.7%; Score 26; DB 6; Length 285
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR PILING DATE: 1999-12-27
PRIOR PILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR PILING DATE: 1099-12-29
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 49
SOFTWARER: PARCENTIN VET: 2.0
SEQ ID NO 42
LENGTH: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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; ORGANISM: Homo sapiens
US-10-701-283-12
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Best Local Similarity
Matches 4; Conserv
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2 AVDIEY 7
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1 SVDVEY 6

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Gaps

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Query Match
Best Local Similarity 100.0
Matches 5; Conservative
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Best Local Similarity 66.73
Matches 4; Conservative
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193 AVDIEY 198
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US-10-415-182A-2698
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                                                                                                                                                                                                           Sequence 40092, Application US/10425114A

Sequence 40092, Application US/10425114A

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Adaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5313) B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT APPLICATION NUMBER: US/10/425,114A
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 40092
LENGTH: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screi, Steven E
APPLICANT: Screi, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: NUCLeic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64094
LENGTH: 241
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86.7%; Score 26; DB 5; Length 316; 66.7%; Pred. No. 2.3e+03; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.7%; Score 26; DB 6; Length 341; 100.0%; Pred. No. 2.4e+03; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: LIB3354-084-A4_FLI.pep US-10-425-114A-64094
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US-10-425-114A-40092
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US-10-425-114A-64094
'Sequence 64094, Application US/10425114A
'GENERAL INFORMATION:
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Best Local Similarity 66.77
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Matches 5; Conservative
                                          4; Conservative
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185 SVDIDY 190
  Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                  1 SVDVEY 6
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ORGANISM: Zea mays
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US-10-425-114A-40092
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208 VDVEY 212

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Sequence 5786, Application US/10739930
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
FILE REPERENCE: 38-21 (53377) B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT APPLICATION NUMBER: US/10/739,930
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 5786
LENGTH: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 447, Application US/60479962

Sequence 447, Application US/60479962

GENERAL INFORMATION:
APPLICANT: Laurie, Cathy C
APPLICANT: Eduark, John R
APPLICANT: Ebait, Brandon J
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Protein in Plants
FILE REPRENEUR: 38-21(53372)A
CURRENT APPLICATION NUMBER: US/60/479,962
CURRENT FILING DATE: 2003-06-19
NUMBER: OF SEQ ID NOS: 488
SOFTWARE: PatentIn version 3.2
SEQ ID NO 447
LENGTH: 442
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         ) ORGANISM: Homo sapiens
) FEATURE:
) NAME/KEY: misc_feature
) CTHER INFORMATION: Incyte ID No: LI:200704.1.orf3:2001MAY17
US-10-473-040-683
                                                                                                                                                                                       Score 26; DB 6; Length 428;
Pred. No. 2.6e+03;
2; Mismatches 0; Indels
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100.0%; Pred. No. 2.6e+03;
tive 0; Mismatches 0; Indels
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OTHER INFORMATION: Clone ID: ARATH-23APR03-C14066_1.p

US-10-739-930-5786
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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398 SIDLEY 403
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              1 SVDVEY 6
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ORGANISM: Zea mays
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APPLICANT: LAN, RAKHAHA, MACHAELE,
APPLICANT: LAN, RULH Y.; URASHKA, MACHAELE
FILE REFRERENCE: PT-1231 USN
CURRENT APPLICATION UNDER: US/10/473,040
CURRENT APPLICATION UNDER: US/10/473,040
FRIOR PILING DATE: 2003-09-26
PRIOR PILING DATE: 2003-03-27
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-05-16
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2001-06-17
PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-20
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APPLICANT: INCYTEC.

APPLICANT: JONES, Anissa L.; TRAN, Alanna-Phung B.;

APPLICANT: JONES, Anissa L.; TRAN, Alanna-Phung B.;

APPLICANT: CHINN, JOYCE; DUFOUR, GERAIG E.;

APPLICANT: CHINN, JONIER L.; YU, Jimmy Y.;

APPLICANT: JAKSON, Olivia; YAP, Pierre E.;

APPLICANT: ANSHEY, Stefan R.; DAUGHERTY, Sean C.;

APPLICANT: DAW, Tam C.; LIU, Tommy F.;

APPLICANT: MOTHEN, DUY-Viet A.; KLEEFELD, Yael;

APPLICANT: GERSTIN, JR., Edward H.; PERALTA, Careyna H.;

APPLICANT: CHEN, Alice J.; PENIS, Samantha A.;

APPLICANT: HARRIS, Bernard; MULLAHY-FLORES, Vincent Z.;

APPLICANT: MARWAHA, Rakesh; LO, Audrey;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.7%; Score 26; DB 6; Length 420
66.7%; Pred. No. 2.6e+03;
.ive 2; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/10/415,182A
CURRENT FILING DATE: 2003-12-09
PRIOR APPLICATION NUMBER: GB-0026333.5
PRIOR FILING DATE: 2000-10-27
PRIOR PLING DATE: 2000-11-24
PRIOR PLING DATE: 2000-11-24
PRIOR PLING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 12024
SEQ ID NO 2696
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     , OKGANISM: Streptococcus agalactiae
US-10-415-182A-2698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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205 AVDIEY 210
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LENGTH: 428
TYPE: PRT
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Query Match
Best Local Similarity 66.7'
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CORGANISM: Glycine max
US-10-679-063-2707
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204 AVDIEY 209
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US-10-451-168-56
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GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
ITTLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026926WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSGENC PLANTS WITH IMPROVED PHENOTYPES
TITLE OF INVENTION: TRANSGENCE BLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15 (22054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 16687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2191. Application US/10679063
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITL OP INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
TITL OP INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15 (5.2054) B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.7%; Score 26; DB 6; Length 460; 100.0%; Pred: No. 2.7e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.7%; Score 26; DB 6; Length 532; 66.7%; Pred. No. 2.8e+03; Live 2; Mismatches 0; Indels
 0; Indels
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CTHER INFORMATION: unsure at all Xaa locations US-10-679-063-2191
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
, ORGANISM: Magnetospirillum magnetotacticum
US-10-679-063-16687
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Best Local Similarity 66...
A; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
 5; Conservative
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                                                              345 VDVEY 349
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42 VDVEY 46
                                   2 VDVEY 6
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                                                                                                                                   RESULT 35
US-10-679-063-16687
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US-10-472-928-3056
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US-10-679-063-2191
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 Matches
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APPLICANT:
TILE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOOO728
CURRENT APPLICATION NUMBER: US/09/614,150A
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-24
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR FILING DATE: 2000-03-23
NUMBER OF SQU ID NOS: 43008
SOFTWARE: FRASERQ for Windows Version 4.0
SEQ ID NO 18810
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al:
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PRILING DATE: 1999-10-12
PRIOR PLING DATE: 1999-10-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-28
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/19,637
PRIOR PLING DATE: 2000-02-3
NUMBER OF SEQ ID NOS: 43008
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          Sequence 18810, Application US/09614150A
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: DROSOPHILA
US-09-614-150A-18810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 606;
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66.7%; Pred. No. 2.9e+03;
cive 2; Mismatches 0,
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Sequence 57, Application US/10451168
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: GLAXO GROUP LIMITED
ITILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GF50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT APPLICATION NUMBER: CO/256,710
PRIOR APPLICATION NUMBER: CO/256,710
PRIOR FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/266,92
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,97
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,97
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-07
PRIOR FILING 
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-04-04
PRIOR PILING DATE: 2001-04-04
PRIOR PILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Homo sapiens
US-10-451-168-56
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ORGANISM: Homo sapiens
US-10-451-168-57
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576 SIDLEY 581
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US-09-614-150A-18810
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Sequence 167, Application US/10475292

GENERAL INFORMATION:

APPLICANT: AI XioLan et al.

TITLE OF INVENTION: PRIMARY NUCLECTIDE SEQUENCE OF THE

TITLE OF INVENTION: AGROITS SEGETUM GRANULOSIS VIRUS (AsGV), INSECTICIDE

TITLE OF INVENTION: ADD CONTROLLING KITS FOR AGROITS SEQUENCE AND PREVENTION:

TITLE OF INVENTION: SPREAD

TITLE OF INVENTION: SPREAD

FILE REFERENCE: CL001308-US

CURRENT APPLICATION NUMBER: US/10/475,292

CURRENT FILING DATE: 2003-10-20

PRIOR APPLICATION NUMBER: PCT/US01/32153

PRIOR PLING DATE: 2001-10-17

PRIOR PILING DATE: 2001-0-18

NUMBER OF SEQ ID NOS: 217

NUMBER OF SEQ ID NOS: 217

LENTH: 883
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APPLICANT: BARR, IAN G.
APPLICANT: BARR, IAN G.
APPLICANT: PATTERSON, MICHELLE A.
APPLICANT: AGIUS, CATHERINE T.
APPLICANT: ROTHEL, LINDA J.
APPLICANT: MARGETTS, MAL B.
APPLICANT: MARGETTS, MAL B.
APPLICANT: HOCKING, DIANNA M.
APPLICANT: HOCKING, DIANNA M.
TITLE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
FILE REFERRNCE: 4137-3
                                   Gaps
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66.7%; Pred. No. 3.3e+03;
ive 2; Mismatches 0; Indels
                                   IndelB
            Pred. No. 3e+03;
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CURRENT FILING DATE: 2000-06-28
PRIOR PELING DATE: 1908-01023
PRIOR PILING DATE: 1998-12-10
PRIOR PILING DATE: 1997-12-10
PRIOR PILING DATE: 1997-12-10
PRIOR APPLICATION NUMBER: AU PP 0839
PRIOR APPLICATION NUMBER: AU PP 182
PRIOR APPLICATION NUMBER: AU PP 1846
PRIOR PILING DATE: 1997-12-31
PRIOR APPLICATION NUMBER: AU PP 2264
PRIOR FILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: AU PP 2911
PRIOR PILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-33
PRIOR APPLICATION NUMBER: AU PP 3338
PRIOR PELING DATE: 1998-04-39
PRIOR PELING DATE: 1998-04-33
100.0%; Prec. ....
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Best Local Similarity 66.7
Matches 4; Conservative
                                   5, Conservative
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     Best Local Similarity
Matches 5, Conserv
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                                                                               2 VDVBY 6
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US-09-581-286A-442
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US-10-475-292-167
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Sequence 42, Application US/10418861B

GENERAL INFORMATION:
APPLICANT: Farah, Shaker Chuck
APPLICANT: Reinach, Fernando de Castro
APPLICANT: Reinach, Fernando de Castro
APPLICANT: De Laia, Marcelo Luiz
APPLICANT: De Laia, Marcelo Luiz
APPLICANT: Setubal Joan C.
APPLICANTON NUMBER: US/10/418,861B
CURRENT FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 42
LENGTH: 676
LENGTH: 676
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 168, Application US/60495589

GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Hillman, Jeffrey D.
APPLICANT: Handdield, Martin
TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTI
TITLE OF INVENTION: DIAGNOSIS, TREATMENT, AND MONITORING OF PERIODONTAL DISEASES
TITLE OF LING DATE: 2003-08-15
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 354
SOFTWARE: Patentin version 3.1
SEQ ID NO 168
LENGTH: 673
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                                                                                                                                                    86.7%; Score 26; DB 5; Length 633; 66.7%; Pred. No. 3e+03; ive 2; Mismatches 0; Indels
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                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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ORGANISM: Xanthomonas
                                                     TYPE: PRT ORGANISM: DROSOPHILA
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Best Local Similarity
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                                                                                    ; ORGANISM: DROSOU
US-09-614-150A-3981
                                                                                                                                                                                                                                                                                                                                                                               RESULT 43
US-60-495-589-168
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US-10-418-861B-42
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     SEQ ID NO 3981
LENGTH: 633
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US-09-614-150A-16857
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APPLICAMT: ROSS, BRUCE C.
APPLICAMT: ROSS, BRUCE C.
APPLICAMT: PATTERSON MICHELLE A.
APPLICAMT: PATTERSON, MICHELLE A.
APPLICAMT: AGIUS, CATHERINE T.
APPLICAMT: AGIUS, CATHERINE T.
APPLICAMT: MARGETTS, MAL B.
APPLICAMT: MEBB. ELIZABETHA M.
APPLICAMT: WEBB. ELIZABETHA M.
APPLICAMTON NUMBER: US/09/581,286A
CURRENT FILING DATE: 1999-12-10
FRIOR PLING DATE: 1999-12-10
FRIOR APPLICATION NUMBER: AU PP 186
FRIOR APPLICATION NUMBER: AU PP 2264
FRIOR APPLICATION NUMBER: AU PP 2264
FRIOR FILING DATE: 1998-03-10
FRIOR APPLICATION NUMBER: AU PP 3128
FRIOR FILING DATE: 1998-03-10
FRIOR APPLICATION NUMBER: AU PP 3128
FRIOR FILING DATE: 1998-03-10
FRIOR FILING DATE: 1998-03-10
FRIOR FILING DATE: 1998-05-05
FRIOR FILING DATE: 1998-05-05
FRIOR FILING DATE: 1998-05-05
FRIOR FILING DATE: 1998-05-05
FRIOR FILING DATE: 1998-07-29
FRIOR APPLICATION NUMBER: AU PP 347
FRIOR FILING DATE: 1998-07-29
FRIOR FILING DATE: 1998-07-29
FRIOR APPLICATION NUMBER: AU PP 347
FRIOR APPLICATION NUMBER: AU PP 348
FRIOR APPLICATION NUMBER: AU PP
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PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: AU PP 3654
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 721
SOFTWARE: Patentin version 3.2
SEQ ID NO 442
LENGTH: 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.7%; Score 26; DB 5; I
66.7%; Pred. No. 3.3e+03;
iive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 316, Application US/09581286A, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Porphyromonas gingivalis US-09-581-286A-442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT (CREANISM: Porphyromonas gingivalis US-09-581-286A-316)
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Best Local Similarity 66.7
Matches 4; Conservative
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451 TVDIEY 456
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1 SVDVEY 6

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APPLICANT:
ITTLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
ITTLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
ITTLE OF INVENTION: DROSOPHILA GENES.
ITTLE OF INVENTION NUMBER: US/09/614,150A
CURRENT APPLICATION NUMBER: 00/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-28
PRIOR PAPLICATION NUMBER: 60/161,932
PRIOR PAPLICATION NUMBER: 60/164,769
PRIOR PLING DATE: 1999-11-12
PRIOR PAPLICATION NUMBER: 60/175,693
PRIOR PLING DATE: 1999-11-2
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-03-23
NUMBER: 60/191,637
PRIOR PLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRASESC FOR WINDOWS VERSION 4.0
SEQ ID NO 16857
LENGTH: 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-614-150A-18237

Sequence 18237, Application US/09614150A

Sequence 18237, Application US/09614150A

Sequence 18237, Application US/09614150A

APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DESCOPPLIA GENES.

FILE REFERENCE: CL000728

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRENT PILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR FILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-28

PRIOR FILING DATE: 1999-11-28
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Sequence 16857, Application US/09614150A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: DROSOPHILA
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US-10-472-928-972
i Sequence 972. Application US/10472928
i GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TILLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
TILLE REPERRNCE: P026926WO
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2003-09-26
PRIOR PILING DATE: 2003-09-26
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SeqWin99, version 1.03
LENGTH: 50
                                                                                                                                                                                                                                                                                                       Gaps
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O
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83.3%; Score 25; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: RestSEQ for Windows Version 4.0
SEQ ID NO 18237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Streptococcus pneumoniae
FEATURE:
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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122 TVDIEY 127
                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-18237
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Search completed: January 20, 2004, 14:01:56 Job time : 25 secs

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Sequence 5, Appliance of Applia
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Sequence 1, Appli
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                                                                                                                                  , Search time 173 Seconds (without alignments) 31.558 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pending Patents_AA Main:*

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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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                                                                                                                                      January 20,
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score
and is
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Maximum DB
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                US-09-1919-703-5

JENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Karystal, Gerald

APPLICANT: Rarystal, Simon W.

TITLE OF INVENTION: Peptides and Their Use to Ameliorate;

TITLE OF INVENTION: Peptides and Their Use to Ameliorate;

TITLE REFERENCE: 50216/003004

CURRENT FILING DATE: 1099-04-19

PRIOR PELICATION NUMBER: US 09/294,457

PRIOR APPLICATION NUMBER: US 09/294,457

PRIOR PILING DATE: 1999-04-19

PRIOR PILING DATE: 1999-04-19

PRIOR FILING DATE: 1995-12-06

NUMBER: OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 16
                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-567-943-5

| Sequence 5, Application US/08567943
| Sequence 5, Application US/08567943
| SEQUENCE 5, Application US/08567943
| APPLICANT: Krystal, Gerald
| TILLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO TITLE OF INVENTION: AMELIORATE CELL DEATH
| NUMBER OF SEQUENCES: 12
| CORRESPONDENCE ADDRESS: | ADDRESSE: SEED and BERRY | STREET: 6300 Columbia Center, 701 Fifth Avenue | CITY: Seattle | STATE: Washington | COUNTRY: US
                                                                                                                                                                                     100.0%; Score 30; DB 24;
100.0%; Pred. No. 5.3e+06;
tive 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                 CTHER INFORMATION: Synthetic polypeptide US-09-919-703-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Synthetic polypeptide US-09-919-703-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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     Sequence 3, Appli
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APPLICANT: Kryerian, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/003004
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT FILING DATE: 2001-07-31
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1996-12-05
PRIOR FILING DATE: 1996-12-05
PRIOR FILING DATE: 1995-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 9; Length 6; Pred. No. 5.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                          APPLICANT: Rabkin, Simon W.
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELIORATE CELL DEATH
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
                                                                                                                                                                                                                                                                                                    5: SEED and BERRY
6300 Columbia Center, 701 Fifth Avenue
     US-09-919-703-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                           ALIGNMENTS
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US-09-919-703-1
Sequence 1, Application US/09919703
GENERAL INFORMATION:
                                                                                                                                                     Sequence 1, Application US/08567943 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 6; Conservative 0;
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STRANDEDNESS: single
TOPOLOGY: linear
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Gaps
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                                                                                                                                                                                                                                                                                                                          Sequence 6. Application US/09919703

GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
APPLICANT: Krystal, Gerald
APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/003004
CURRENT APPLICATION WUMBER: US/09/919,703
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1999-04-19
PRIOR FILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 20
                                            100.0%; Score 30; DB 9; Length 20; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rabkin, Simon W.
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELIORATE CELL DEATH
NUMBER OF SEQUENCES: 12
CORRESPONDENCE SIDES ADDRESSES: SEES SEES SEES ADDRESSES: SEES AND SERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CTRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,943
FILING DATE: 06-DEC-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08567943 GENERAL INFORMATION:
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NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                            Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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STATE: Washington
                                                                                                                                                        1 SVDVEY 6
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100.0%; Score 30; DB 9; Length 18;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,943
FILING DATE: 06-DEC-1995
CLASSIFCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MORRESTER TO BOY DD.
FREINGTHON NUMBER: 780059.401A1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08567943
GENERAL INFORMATION:
APPLICANT: Rabkin, Simon W.
APPLICANT: Rabkin, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELIORATE CELL DEATH
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
CONTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC Compatible
COMPUTER: IB PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,943
FILING DATE: 06-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTEERS DAVIG D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 780059.401A1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 780059.401A1
TELECOMMUNICATION INFORMATION:
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TELEFAX: (206) 682-6031
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-567-943-6
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Sequence 104246, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Blonomix, Inc.
APPLICANT: Blonomix, Inc.
APPLICANT: Danzer, Joseph
ITILE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB)
ITILE OF INVENTION: METHODS OF USE THEREOF
ITILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 104448
LENGTH: 138
TYPE: PRT.
CORGANISM: pdb 1QQRA
US-09-791-537-104248
                                                                                                                                                                                                                                                                                                                                                               Sequence 12562, Application US/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: WETHOOS OF USE THEREOF
TITLE OF INVENTION: METHOOS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE PATENTIN VERSION 3.0
SEQ ID NO 12562
LENGTH: 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 30; DB 22; Length 138; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels (
                                                                                                                    Score 30; DB 22; Length 128; Pred. No. 1.3e+02;
                                                                                                                                                                0; Indels
                                                                                                                                                                0; Mismatches
                         TYPE: PRT ; ORGANISM: Streptococcus pyogenes US-09-791-537-83460
                                                                                                                    100.0%;
                                                                                                               Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: pdb 1C4PA
US-09-791-537-12562
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US-09-791-537-12562
         LENGTH: 128
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VETSION 3.0
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GENERAL INCORMATION:
APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/00304
CURRENT APPLICANTON NUMBER: US/09/919,703
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT PILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR FILING DATE: 1999-04-19
PRIOR PILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 7
SEQ ID NO 7
LEASTH APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 7
LEASTH APPLICATION NUMBER: US 06/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 7
LEASTH APPLICATION NUMBER: US 06/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 7
LEASTH APPLICATION NUMBER: US 06/008,233
PRIOR PILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
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REFERENCE/DOCKET NUMBER: 780059.401A1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: 372836
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTER.STICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                   TOPOLOGY: linear
US-08-567-943-7
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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US-09-791-537-83460
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US-09-919-703-7
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GENERAL INFORMATION:
APPLICANT: Rabkin, Simon W.
APPLICANT: Krystal, Gerald
ITILE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELICRATE CELL DEATH
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Madrazo, Isis Del Carmen Torrens
APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Menendez, Aliana Seralena
APPLICANT: Manendez, Aliana Seralena
APPLICANT: Becalona, Elder Pupo
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILER REFERENCE: Sequence Listings 1-14 re: 976-5
CURRENT APPLICATION NUMBER: US/09/658,681
CURRENT APLICATION NUMBER: 2000-09-08
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 30; DB 20; 100.0%; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/658,681
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 384
TYPE: PT.
CORGANISM: Streptococcus equisimilis
US-09-658-681-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-681-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09658681 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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ZIP: 98104-7092
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SEQ ID NO 1
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          Sequence 23287, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Madrazo, Isis Del Carmen Torrens
APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Ojalvo, Ariana Garcia
APPLICANT: Ojalvo, Ariana Garcia
APPLICANT: Menendez, Alina Seralena
APPLICANT: Bscalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
ITILE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14 re: 976-5
CURRENT APPLICATION NUMBER: US/09/658,681
CURRENT APPLICATION NUMBER: 100-09-08
NUMBER OF SEQ ID NOS: 14
SSEQ ID NOS: 14
SSEQ ID NO 3: 12
LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 30; DB 22;
100.0%; Pred. No. 4.6e+02;
ive 0; Mismatches 0;
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APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Garcia, Ariana Garcia
APPLICANT: Menendez, Alina Sacralena
APPLICANT: Escalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREFPOKIRASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14 re: 976-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/09658681
; GENERAL INFORMATION:
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; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: pdb 1BMLC
US-09-791-537-23287
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Matches 6; Conserv
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LENGTH: 362
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US-09-658-681-4
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Gaps

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Sequence 264, Application US/10360101

Sequence 264, Application US/10360101

Sequence 261, Application US/10360101

APPLICANT: Moll, Gert N.

APPLICANT: Moll, Gert N.

TITLE REPERBACE: 2183-5673

CURRENT FILING DATE: 2003-02-07

PRIOR PELICATION NUMBER: EP 02077066.8

PRIOR PELICATION NUMBER: EP 02077066.8

PRIOR FILING DATE: 2002-05-24

NUMBER: Patentin version 3.1

SEQ ID NO 264

LENGTH: 413
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GENERAL INFORMATION:

HAPLICANT: Reed, Guy L.

TILLE OF INVENTION: Deptides Specifically Binding to Plasminogen And the TILLE OF INVENTION: Deptides Such Peptides

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEB: Sterne, Keseler, Goldstein and Fox STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 30; DB 24; Length 413; 100.0%; Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 30; DB 29; Length 413; 100.0%; Pred. No. 5.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: sequence of streptokinase US-10-360-101-264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR PILLING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILLING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 413
                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Synthetic polypeptide US-09-919-703-12
                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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PCT-US93-09502-1
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                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 30; DB 9; Length 413; Best Local Similarity 100.0%; Pred. No. 5.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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SEQUENCE 12, APPLICATION

GENERAL INFORMATION:

APPLICANT: Kryetal, Gerald

APPLICANT: Kryetal, Gerald

TITLE OF INVENTION: Peptides and Their Use to Ameliorate

TITLE OF INVENTION: Call Death

FILE REFERENCE: 50216/003004

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 09/294,457

PRIOR PILING DATE: 1999-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-658-681-2

JOS-09-658-681-2

JOSERAL INFORMATION:

APPLICANT: Madrazo, Isis Del Carmen Torrens

APPLICANT: Garcia, Jose De Jesus De La Fuente

APPLICANT: Ojalvo, Ariana Garcia

APPLICANT: Menendez, Alina Seralena

APPLICANT: Masso, Julio Raul Fernandez

APPLICANT: Masso, Julio Raul Fernandez

APPLICANT: Griego, Marcha De Jesus Gonzalez

TITLE OF INVENTION: STREPTOKINASE MUTANTS

FILE REFERENCE: Sequence Listings 1-14 re: 976-5

CURRENT FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1

LENGTH: A.
  APPLICALL...
FILING DATE: 06-DEC----
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCAMBER: 33,963
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 780059.401A1
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEFACHOE: 2060 622-4900
TELEFACHOE: 3723836
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 413 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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APPLICANT: Reed, Guy L.
TITLE OF INVENTION: Peptides Specifically Binding to Plasminogen And the TITLE OF INVENTION: DNA Encoding Such Peptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox
STREST: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: Patentin Release #1.0, Version #1.25
SOUTHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/128,299
FLING DATE: Herewith
CLASSIFICATION 435
ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.;
REFERENCE/DOCKET NUMBER: 0609.3570001
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2545
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENETAL 414 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 30; DB 5; L
100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr L.L.P.
STREET: 60 State Street
                                                                                                                                                                  Sequence 1, Application US/08128299 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
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TYPE: amino acid
STRANDEDNESS: both
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Matches 6, Conservative
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                                                             157 SVDVEY 162
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US-09-438-136-252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Read, Guy L.

APPLICANT: Read, Guy L.

APPLICANT: Read, Guy L.

APPLICANT: Read, Guy L.

APPLICANT: Parhami-Seren, Behnaz

TITLE OF INVENTION: Decreased Antigenicity and Uses Thereof

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSE: Sterne, Kessler, Goldstein and Fox

STREET: 1225 Connecticut Avenue

STREET: D.C.

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

EDIT 2003

EDIT 2003

COMPUTER READABLE FORM:

COMPUTER: IBM FOC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/956,692A

FILING DATE: 19921005

CURRENT APPLICATION HATA:

APPLICATION NUMBER: US/07/956,692A

FILING DATE: 19921005

ATORNEY/AGENT INFORMATION:

NAME: Goldstein, Jorge A.

REFERENCE/DOCKET 1009

FREFERENCE/DOCKET 1009

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 833-7533

TELEPHONE: (202) 833-753

TELEPAX: (202) 833-753

TELEPAX: (202) 833-753

TELEPAX: 414 amino acids
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09502
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                  0609.3570001
                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2545
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER.STICS:
LENGTH: 414 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 414 amino acids
AMINO ACID
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Best Local Similarity 100...
6. Conservative
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Best Local Similarity 100.0
Matches 6; Conservative
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US-07-956-692A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21.
US-07-953-692A-9
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APPLICANT: Sahni, Girish
APPLICANT: Kumar, Rajesh
APPLICANT: Roy, Chaiti
APPLICANT: Roy, Chaiti
APPLICANT: Rajagopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Deepak
APPLICANT: Sundaram, Vasudha
APPLICANT: Yadav, Mahavir
TITLE OF INVENTION: PLASMINGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF SAID PROTEINS
FILE REFERENCE: 07064/009001
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100.0%; Pred. No. 5.40+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 30; DB 18;
100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 102286.395CON
TELECOMMUNICATION INFORMATION:
                                                                                                            APPLICATION NUMBER: GB 9725270.4
FILING DATE: 28 NOV-1997
APPLICATION NUMBER: GB 9807751.4
FILING DATE: 14-APR-1998
APPLICATION NUMBER: US 60/067,235
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: BAKET, HOllie L.
REGISTRATION NUMBER: 31,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/471,349
CURRENT FPLING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US/09/471,349
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 414
                                                                     APPLICATION NUMBER: GB 9716197.0 FILING DATE: 31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
SEQUENCE DESCRIPTION: SEQ ID NO: 253:
US-09-438-136-253
                                9710480.6
                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 526-6000 INFORMATION FOR SEQ ID NO: 253:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus equisimilis US-09-471-349-2
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US-09-633-516B-7
; Sequence 7, Application US/09633516B
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GENERAL INFORMATION:
APPLICANT: Sahni, Girish
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 414 amino acids
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,136
FILING DATE: 10-Nov-1999
CLASSIFCATION NUMBER: WO PCT/GB98/01473
FILING DATE: 21-MAY-1998
APPLICATION NUMBER: GB 9710480.6
FILING DATE: 21-MAY-1997
APPLICATION NUMBER: GB 9716197.0
FILING DATE: 31-JUL-1997
APPLICATION NUMBER: GB 9725270.4
FILING DATE: 28-NOV-1997
APPLICATION NUMBER: GB 9807751.4
FILING DATE: 14-APR-1998
APPLICATION NUMBER: B 9807751.4
FILING DATE: 14-APR-1998
APPLICATION NUMBER: US 60/067,235
ATTORNEY/AGENT INFORMATION:
NAME: Baker, HOllie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102286.395CON
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109

COMPUTER READABLE FORM:

MEDION TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/438,136

FILING DATE: 10-Nov-1999

CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 253, Application US/09438136
GENERAL INFORMATION:
GENERAL INFORMATION:
CARTER, Francis Joseph
HAMILTON, Anita Anne
CARTER, Graham
TITLE OF INVENTION: NETHOD FOR THE PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/GB98/01473
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SEQUENCE DESCRIPTION: SEQ ID NO: 252:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr L.L.P.
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 526-6000 INFORMATION FOR SEQ ID NO: 252:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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Best Local Similarity
Matches 6; Conserva
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US-09-438-136-253
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APPLICANT: Debe, Derek
HAPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB:
TITLE OF INVENTION: WETHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
LEMOTH: 414
TYPE:
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Sequence 2, Application US/09940235

Sequence 2, Application US/09940235

GENERAL INFORMATION:

APPLICANT: Sahni, Girish
APPLICANT: Rajegopal, Kammara
APPLICANT: Nihalani, Deepak
APPLICANT: Nihalani, Vasudha
APPLICANT: Nihalani, Vasudha
APPLICANT: Novel CLOT-SPECIFIC STREPTOKINASE
ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
ITILE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
ITILE OF INVENTION: PROTEINS PROTEINS PROFESSING ALTERED PLASMINOGEN ACTIVATION
ITILE OF INVENTION: PROTEINS PROFESSING ALTERED PLASMINOGEN ACTIVATION
ITILE OF INVENTION: PROTEIN PROTEINS PROFESSING ALTERED PLASMINOGEN ACTIVATION
ITILE OF INVENTION: PROTEIN PROFESSING ALTERED PLASMINOGEN ACTIVATION
ITILE REPERENCE: 07064-009002
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100.0%; Pred. No. 5.4e+02;
ive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
APPLICANT: ADAIR, Fions Suzanne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: CARTER, GRADAM
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT FILING DATE: 2002-04-09
PRIOR PELLING DATE: 1999-12-23
FRIOR FILING DATE: 1999-12-23
FRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Streptococcus equisimilis US-09-791-537-418
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Best Local Similarity 100.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                      APPLICANT: Financia Joseph CARR
APPLICANT: Fiona Suzanne ADAIR
APPLICANT: Anica Anne HAMILTON
APPLICANT: Anica Anne HAMILTON
APPLICANT: Anica Anne HAMILTON
APPLICANT: Anica Anne HAMILTON
TITLE OF INVENTION: Modifying Protein Immunogenicity
TITLE OF INVENTION: Modifying Protein Immunogenicity
CURRENT APPLICATION NUMBER: US/09/633,516B
2000-08-04
CURRENT FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: GB9902139.6
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: GB9902139.6
PRIOR APPLICATION NUMBER: GB9902139.6
PRIOR FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Froncis Joseph CARR
APPLICANT: Frona Suzanne ADAIR
APPLICANT: Anica Anne HAMILTON
APPLICANT: Anica Anne HAMILTON
APPLICANT: Anica Anne HAMILTON
TILLE OF INVENTION: Modifying Protein Immunogenicity
FILE REPERENCE: 112408-120
CURRENT APPLICATION NUMBER: US/09/633,516B
2000-08-04
CURRENT APPLICATION NUMBER: PCT/GB99/04119
PRIOR APPLICATION NUMBER: GB992695.1
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1998-12-08
SOFTWARE: PATCHING DATE: 1999-02-02
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US-09-791-537-418
; Sequence 418, Application US/09791537
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus equisimilis
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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US-10-611-558-2

Sequence 2 Application US/10631558

GENERAL INFORMATION:

APPLICANT: Rainar, Raiesh

APPLICANT: Sahni, Girish

APPLICANT: Sahni, Girish

APPLICANT: Rajagopal, Kammara

APPLICANT: Rajagopal, Kammara

APPLICANT: Nahalari, Deepak

APPLICANT: Nahalari, Deepak

APPLICANT: Nadavim Vasudha

APPLICANT: Nadavim NOVEL CLOT-SPECIFIC STREPTOKINASE

TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID

TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION

TITLE OF INVENTION: US/10/631,558

CURRENT FILING DATE: 2003-07-31

PRIOR APPLICATION NUMBER: US/09/940,235

PRIOR APPLICATION NUMBER: US/09/940,235

PRIOR FILING DATE: 1999-12-24

** NUMBER: OF SEQ ID NOS: 28

** SOFTWARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 414

TWOS: DATE: 1919
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APPLICANT: Zhang, Xuejun C
APPLICANT: Zhang, Jozdan
TITLE OF INVENTION: Thrombolytic Agents Derived from Streptokinase
TITLE REFERENCE: OMRF 173
FILE REFERENCE: OMRF 173
FILE REFERENCE: OMRF 173
CURRENT TAPLICATION WUMBER: US/09/305,958
CURRENT TILING DATE: 1998-05-06
EARLIER APPLICATION WUMBER: 60/084,392
EARLIER FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 415
TYPE: PRT
CORANIEM: Streptococcus sp.
                                 Gaps
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                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 30; DB 31; 100.0%; Pred. No. 5.4e+02;
   Pred. No. 5.4e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ), ORGANISM: Streptococcus equisimilis US-10-631-558-2
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; Sequence 4, Application US/09305958
; GENERAL INFORMATION:
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NAME/KEY: PEPTIDE
CCATION: (1)...(415)
CTHER INFORMATION: Etreptokinase
US-09-305-958-4
100.08;
   Best Local Similarity 100. Matches 6; Conservative
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Best Local Similarity 100.
Matches 6, Conservative
                                                                                                                                     157 SVDVEY 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-500-415-253, Application US/10300215
GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
APPLICANT: ADAIR, Fiona Suzanne
APPLICANT: ADAIR, Fiona Suzanne
APPLICANT: HAMITON, Anita Anne
APPLICANT: HAMITON, MITHAD FOR THE PRODUCTION OF
TITLE OF INVENTION: NON-IMMONGENIC PROTEINS
FILE REFERENCE: MER-104-Con.1
CURRENT APPLICATION NUMBER: US/10/300,215
CURRENT ILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1997-05-21
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-05-21
PRIOR FILING DATE: 1997-05-21
PRIOR FILING DATE: 1997-05-21
PRIOR FILING DATE: 1997-05-21
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-11-28
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 254
NUMBER OF SEQ ID NOS: 254
MUNDER OF SEQ ID NOS: 254
                                                                                      CURRENT FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US 09/438,136
PRIOR PILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: W0 PCT/GB98/01473
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1997-05-21
PRIOR PILING DATE: 1997-05-21
PRIOR PILING DATE: 1997-07-31
PRIOR PILING DATE: 1997-07-31
PRIOR PILING DATE: 1997-11-28
PRIOR PILING DATE: 1997-11-28
PRIOR PILING DATE: 1997-11-28
PRIOR PILING DATE: 1997-11-28
PRIOR APPLICATION NUMBER: GB 9807751-4
PRIOR APPLICATION NUMBER: US 60/067,235
PRIOR PILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FastSEQ for Windows Version 4.0
   TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Modified strep protein US-10-300-215-253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Streptococcus equisimilis US-10-300-215-252
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Best Local Similarity 100.
Matches 6; Conservative
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DB 29; Length 414;

100.0%; Score 30;

Query Match

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Sequence 45187, Application US/09791537

Sequence 45187, Application US/09791537

GREEAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOOTHARE: Patentin version 3.0
SEQ ID NO 45187
LENGTH: 440
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Debe, De
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREB DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERBYCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Ratentin version 3.0
SEQ ID NO 45192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 30; DB 22; Length 440; 100.0%; Pred. No. 5.9e+02;
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; CRGANISM: Streptococcus equisimilis
US-09-791-537-45187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Streptococcus pyogenes US-09-791-537-45189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.(
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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US-09-791-537-45189
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US-09-791-537-45192
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APPLICANT: Dense, Derek
APPLICANT: Dense, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPRENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 32688
LENGTH: 415
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Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
APPLICANT: Lin, Xinli
APPLICANT: Tang, Jordan
TITLE OF INVENTION: Human Plasminogen Activator
TITLE OF INVENTION: Human Plasminogen Activator
FILE REFERENCE: OMRF 175
CURRENT APPLICATION NUMBER: US/09/305,970
CURRENT PILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: 60/110,588
EARLIER FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
ILENGTH: 415
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100.0%; Pred. No. 5.4e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                               RESULT 34
US-09-305-970-5
; Sequence 5, Application US/09305970
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: PEPTIDE
LOCATION: (1)..(415)
OTHER INFORMATION: streptokinase
US-09-305-970-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Streptococcus sp
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 145994
LENGTH: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                         APPLICANT: Martin R.
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Miliamen, Mark
TITLE OF INTENTION: Novel Kinases and Uses Thereof
FILE REFERENCE: MP11999-096CP2
CURRENT APPLICATION NUMBER: US/09/609,360D
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/562,480
PRIOR RILING DATE: 1999-06-30
PRIOR RILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25:
LENGTH: 891
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100.0%; Pred. No. 1.4e+03;
iive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: Novel Kinases and Uses Thereof
FILE REFERENCE: 35800/234862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-791-537-145994
; Sequence 145994, Application US/09791537
; GENERAL INFORMATION:
                                                                                                                                                    Sequence 25, Application US/09609360D GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: Hydra vulgaris
US-09-791-537-145994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Hydra vulgaris
US-09-609-360D-25
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1 SVDVEY
                                                                                                           RESULT 41
US-09-609-360D-25
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US-09-862-027-25
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                                                                                                      100.0%; Score 30; DB 22; Length 440; 100.0%; Pred. No. 5.9e+02; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 30; DB 20; Length 891;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/09609360B
Sequence 25, Application US/09609360B
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
APPLICANT: Williamson, Mark
TITLE OF INVENTION: Novel Kinases and Uses Thereof
FILE REFERENCE: 35800/200938
CURRENT APPLICATION NUMBER: US/09/609,360B
CURRENT FILING DATE: 2000.11-13
PRIOR FILING DATE: 2000.11-13
PRIOR PILING DATE: 2000.05-01
PRIOR PILING DATE: 2000.05-01
SPRIOR FILING DATE: 2000.05-01
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENTH: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/09609360C

GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
APPLICANT: Hodge, Martin R.
APPLICANT: Majlamson, Mark
TITLE OF INVENTION: Novel Kinases and Uses Thereof
FILE REFERENCE: MP11999-096CP2
CURRENT APPLICATION NUMBER: 09/9609,360C
CURRENT FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PLICATION NUMBER: 09/345,473
PRIOR PLICATION NUMBER: 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
                    ; TYPE: PRT
; ORGANISM: Streptococcus sp
US-09-791-537-45192
                                                                                                      Query Match
Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: Hydra vulgaris
US-09-609-360B-25
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US-09-609-360C-25
                                                                                                                                                                                                                                  183 SVDVEY 188
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 440
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                                                                                                                                                                                                                                       Sequence 234, Application US/60143753
Sequence 234, Application US/60143753
GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
GURRENT APPLICATION NUMBER: US/60/143,753
CURRENT APPLICATION NUMBER: US/60/143,753
CURRENT PILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 234
LENGTH: 43
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) Sequence 236, Application US/60145989
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ION CHANNEL PROTEINS, AND USES;
TITLE OF INVENTION: THERROF
FILE REPERENCE: CL000066
GURRENT APPLICATION NUMBER: US/60/145,989
CURRENT APPLICATION NUMBER: US/60/145,989
NUMBER OF SEQ ID NOS: 456
SEQ ID NOS: 456
LENGTH: 66
LENGTH: 66
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           Length 43;
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96.7%; Score 29; DB 32; Length 66;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels
         Query Match 96.7%; Score 29; DB 32; Best Local Similarity 83.3%; Pred. No. 56; Matches 5; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.7%; Score 29; DB 32;
83.3%; Pred. No. 56;
tive 1; Mismatches 0
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ORGANISM: Drosophila
FATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(66)
OTHER INFORMATION: Xaa = Any Amino Acid
US-60-145-989-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
COGANISM: Drosophila
FEATURE:
NAME/KEY: VARIANT
J. LOCATION: (1)...(43)
OTHER INFORMATION: Xaa = Any Amino Acid
US-60-143-753-234
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Best Local Similarity 83.5.
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35 SIDVEY 40
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GENERAL INFORMATION:
APPLICANT: Bloomia, inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC
TITLE OF INVENTION: HERROF
TITLE OF INVENTION: HERROF
FILE REPERENCE: CLO00035
CURRENT APPLICATION NUMBER: US/60/139,670
CURRENT APPLICATION NUMBER: US/60/139,670
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 229
SOFTWARE: PARSEQ for Windows Version 3.0
SEQ ID NO 115
LENGTH: 43
TYPE: PRT
CORGANISM: Drosophila
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CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 891
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LOCATION: (1)...(43)

CTHER INFORMATION: Xaa = Any Amino Acid
US-60-139-670-115
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US-09-791-537-105510
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Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: Hydra vulgaris
US-09-862-027-25
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US-09-791-537-105510
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LENGTH: 1274
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US-60-139-670-115
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Search completed: January 20, 2004, 14:01:20
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Best Local Similarity 83.3
Matches 5, Conservative
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ION CHANNEL PROTEINS, AND USES;
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: WUMBER: US/60/145,989
CURRENT APPLICATION NUMBER: US/60/145,989
CURRENT FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 456
SOFTWARE: FRACEOF FOR Mindows Version 3.0
SOFTWARE: FRACEOF FOR MINDOWS VERSION 3.0
IENGTH: 68
Sequence 515, Application US/60145138

Sequence 515, Application US/60145138

GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00062
CURRENT APPLICATION NUMBER: US/60/145,138
CURRENT FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 948
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 515
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NAME/KEY: VARIANT
LOCATION: (1)...(69)
OTHER INFORMATION: Xaa = Any Amino Acid
US-60-145-138-515
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Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Drosophila
US-60-145-989-317
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38 SIDVEY 43
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US-10-424-599-271681
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US-60-145-989-317
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; SEQ ID NO 271681
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa location8
; FEATURE:
; CATHER INFORMATION: Clone ID: PAT_MRT3847_87347C.1.pep
US-10-424-599-271681
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Pred. No. 1.1e+02;
1; Mismatches 0
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Recombinant strept Peptide correspond Streptokinase from Streptokinase (1-3

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Sequence:

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AAY01550
AAY1558
AAY21568
AAY01557
AAR10159
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AAR10199
AAR10199
AAY2620
AAR10199
AAY2620
AAR20202
AAR20202
AAR20202
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AAY01556
AAW94664
AAW94665
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AAW86144
AAW86144
AAB01295
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AAY50870
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AAW21723
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                                                                     1107863
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                                                                    Total number of hits satisfying chosen parameters:
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ALIGNMENTS

Leptospira membran Galid herpesvirus

Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; cellular differentiation; physical insult; trauma; anoxia; hyperthermia; hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; Huntington's disease; cereballar degeneration; cardiorascular disease; familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; infaction; heart disease; cardiomyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rehematciod arthritis; renal; retinal; systemic lupus erythematosus; insulin-dependent; diabetes mellitus; perfusion injury; immune disease; rougher andogau; myasthenia gravis; perfusion injury; immune disease; entoimanne polyarthritides; systemic lupus erythematosus; insulin-dependent; diabetes mellitus; pernicious anaemia; temporal arthritis; autoimanne polyarthritides; wegener's granulomatosis; glomerulomephritis; anti-phospholipid syndrome; neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma; mon-Hodgkin's Lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; spinal and Bare Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline. Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation Streptokinase derived peptide 1 for amelioration of cell death. peptides derived from Claim 2; Column 12; 15pp; English. AAY25009 standard; peptide; 6 AA 96US-0759599 95US-0008233 96US-0759599 (first entry) AAY25009-Y25019 are novel Krystal G, Rabkin SW; WPI; 1999-394231/33. (RABK/) RABKIN S W. 05-DEC-1996; 23-AUG-1999 06-DEC-1995; 05-DEC-1996; 29-JUN-1999 Synthetic. AAY25009; 

Treptokinase, cell death, apoptosis, necrosis, nootropic, neuroprotective, antiparkinsonian, anticonvulsant; cytostatic, neuroprotective; antiparkinsonian, anticonvulsant; cytostatic; neuroprotectic; vasotropic; immunosuppressive; anti-HIV, dermatological; antidiabetic; intibarestic; neurodegenerative disease; antibacterial; antiparastic; neurodegenerative disease; antibacterial; antiparastic; neurodegenerative disease; whereholds degeneration; neoplastic disease; Huntington's disease; whereholds disease; inflammatory joint disease; antidammatory disease; myocardial reperfusion injury; immune disease, autoimmune disease; myocardial reperfusion injury; immune disease, autoimmune disease; acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis; myelodegenerative diseases; ulcerative colitis; pancreatitis; other organs), ischemia or reperfusion injury (e.g. myocardial ischemia and reperfusion injury, renal ischemia, spinal cord ischemia and/or reperfusion injury, rethal ischemia, or infarction, and stroke), toxic insult (e.g. liver toxicity, lashemia or infarction, and stroke), toxic organs from chemicals, radiation, and other noxious substances), macular degeneration, cataract formation, pancreatitis, Crohn's disease, ulcerative collists, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord, duillan Bare Syndrome and demyelinating disease), bypass surgery, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT, Gaps New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders .. 0 Length 6; Indels ö Score 30; DB 20; Pred. No. 9.3e+05; 0; Mismatches 0; (MOLE-) MOLECULAR THERAPEUTICS INC. ABB80001 standard; peptide; 6 AA. Streptokinase derived peptide#1. Claim 3; Column 5; 18pp; English. 100.0%; 95US-008233P. 26-JUL-2002 (first entry) 6; Conservative prion disease; aging. WPI; 2002-266542/31. and anthracyclines. Query Match Best Local Similarity 9 6 AA; SVDVEY SVDVEY JS6348567-B1. 19-APR-1999; 06-DEC-1995; 05-DEC-1996; 19-FEB-2002. Krystal G, Synthetic. ABB80001; ٦ Sequence Matches RESULT 2 ABB8000 셤 ઠે

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as nootropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antiatherosclerotic, vasotropic, immunosuppressive, anti-HNO described as antiatherosclerotic, vasotropic, immunosuppressive, anti-HNO described as antiulcer, antibacterial and antiparasitic. Peptides of the invention antiulcer, antibacterial and antiparasitic. Peptides of the invention antiulcer, antibacterial and antiparasitic. Peptides of the invention comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. Parkinson's, Altoeimer's, Huntington's disease and cerebellar degeneration) neoplastic disorders including cancer, inflammatory disorders (e.g. arthitis, inflammatory joint cancer, inflammatory disorders (e.g. arthitis, inflammatory joint disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis and myocardial repertusion injury), immune diseases (e.g. heart failure, anterimine), systemic lupus erythematosus, diabetees mellitus, pernicious anaemia), myelodegenerative diseases, viral diseases, and degenerative diseases of any organ. Other disorders include macular degeneration, cataracts, croph, s diseases including bacteria, parasite, prion-based diseases, and accelerated aging. The current sequence repersents a streptokinase defined derived peptide of the invention with an ability to ameliorate cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptokinase, cell death, apoptosis, necrosis, nootropic, neuroprotective, antiparkinsonian, anticonvulsant; cytostatic; antiinflammatory; antiarthritic; antifrhematic; cardiant; antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV; dermatological; antidabetic; antibaressive; anti-HIV; antiulcer; antibacterial, antiparastitc; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; Huntington's disease; Parkinson's disease; Alzheimer's disease; Huntington's disease; Mricardiovascular degeneration; neoplastic disease; Huntington's disease; morazdiovascular disease; arthritis; inflammatory joint disorders; arthritis; inflammatory joint disease; morazdiovascular repertusion injury; immune disease; autoimmune disease; acquired immunodeficiency syndrome; AlDS; rheumatoid arthritis; systemic lupus erythematosus; diabetes mellitus; pernicious anaemia; mellitus; penciative diseases; ulcerative colitis; pancreatitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 30; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80005 standard; peptide; 16 AA.
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96US-0759599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                death in cardiac myocytes.
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Best Local Similarity 100..
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05-DEC-1996;
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peptides or the invention may be described as, nootropic, antinflammatory, antiparkingonian, anticonvulsant, cytostatic, antinflammatory, antiparkingonian, anticonvulsant, cytostatic, antinflammatory, antiparkingonic, immunosuppressive, anti-HIV.

Comprision antibacterial and antiparasitic. Peptides of the invention are useful for treating comprising peptides of the invention are useful for treating comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. parkinson's, Alzheimer's, Huntington's disease and cerebellar degeneration) neoplastic disorders including cancer, inflammatory disorders (e.g. parkinson's, Alzheimer's, Huntington's disease, andiovascular diseases (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune construint in particious and myocardial reperfusion injury), immune diseases (e.g. autoimmune construint in the current sequence represents a streptokinase construint construint in the current sequence construints in the current sequence construints construints in the current construints in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic,
                                                                                                                                                                                                                                           New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders
                                 (MOLE-) MOLECULAR THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Column 5; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    death in cardiac myocytes.
                                                                                                      Rabkin SW;
                                                                                                                                                                            WPI; 2002-266542/31.
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                                                                                                      Krystal G,
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100.0%; Score 30; DB 23; Length 16; 100.0%; Pred. No. 1.9; tive 0; Mismatches 0; Indels 

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Gape .. 0

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AAY25013

Streptokinase derived peptide 5 for amelioration of cell death. AAY25013 standard; peptide; 18 AA. (first entry) 23-AUG-1999 AAY25013;

The Streptokinase, cell death; amelioration; treatment; disease; aging; AIDS; cellular differentiation; physical insult; trauma; anoxia; hyperthermia; hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; Huntington's disease; cerebellar degeneration; cardiovascular disease; W familial amyotrophic lateral solerosis, atheroselerosis; heart failure; M infarction; heart disease; cardiomyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lupus erythematosus; insulin-dependent; diabetes mellitus; W pernicidus anaemia; dermacomyositis; enythema nodosum; myasthenia gravis; Sjogren's syndrome; temporal arthritis; auti-phospholipid syndrome; neoplastic disorder; leukemia; sarcoma; myeloma; neuronma; neuronma; 

RESULT 5

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melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cararact; pancreatitis, Crohn's disease; ulcerative colitis; motor neuron disease; Guillan Bare Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline.
                                                                                          96US-0759599.
                                                                                                      95US-0008233.
96US-0759599.
                                                                                                                                         Krystal G, Rabkin SW;
                                                                                                                                                       WPI; 1999-394231/33.
                                                                                                                           (RABK/) RABKIN S W.
                                                                                          05-DEC-1996;
                                                                                                        06-DEC-1995;
05-DEC-1996;
                                                               US5917013-A.
                                                                            29-JUN-1999.
                                                  Synthetic.
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Claim 6; Column 12; 15pp; English.

ANY SEGONS AT ANY SEGONS ARE NOVED PREDICTED BY The DEFORMER BY THE PRODUCTS of the invention and their encoding muclior acidis may be useful for treating diseases and conditions related to aging, cellular differentiation, physical insult (e.g. physical and trauma, anoxia, hyperthermia, hypothermia, chemically induced damage, and trauma to the brain, spinal cord, xider, hear, lungs, liver, skin and any other organ), viral disorders (e.g. hepatitis, retroviral infections, viral encephalitis, and AIDS/HIV) neurodegenerative disease, cerebellar degenerations, and familial amyotrophic lateral scalerosis (FALS)). Cardiovascular disease, Alzheimer's disease, retroviral scalerosis (FALS), cardiovascular disease, and hypertenators, and hypertenators, and proceedial infarction, heart failure, cardiomyopathy, myocardial corporation, heart failure, cardiomyopathy, myocardial corporation, buyus, pernicious anaemia, dermatomyositis, enythema corporation injury, lupus, pernicious anaemia, dermatomyositis, enythema corporation, sprandiome, temporal arthritis, myasthenia gravis, wegener's granulomatorsis, glomerulonephritis, anti-phospholipid syndrome, the proceeding anaemia, dermatomyositis, enti-phospholipid syndrome, respectivation, and stochamia, myelomas, carcinomas, meromas, melanoma, cancers of the sarcomas, myelomas, carcinomas, melanoma, cancers of the corporation, and inflammatory induced cell damage to the eye, brain and corporate organs permition, renal ischemia or infarction, and stocke, toxic incertivation injury, renal ischemia or infarction, and stocke, toxic insult (e.g. luver toxicity, pulmonary toxicity, toxic damage to other corgans from chemicals, radiation, and other noxious substances; and carrior, cataract formation, panceatitis, coxic damage to other corgans from chemicals, radiation, and other noxious substances), motor chemically induced repetitusion, and chemicals, radiation, and other noxious substances, degeneration, and demerinating diseases, degeneration, and therapeutics such hardy. Cord and an and anthracyclines.

18 AA;

ö Gaps ö 100.0%; Score 30; DB 20; Length 18; 100.0%; Pred. No. 2.2; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100... Fine 6; Conservative

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Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Complex differentiation; physical insult; trauma; anoxia; AIDS; cellular differentiation; physical insult; trauma; anoxia; hyperthermia; hyporthermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; Huntington's disease; cerebellar degeneration; cardiovascular disease; whitington's disease; cerebellar degeneration; cardiovascular disease; milai al amyotrophic lateral sclerosis; heart failure; milai al amyotrophic lateral sclerosis; heart failure; milaretion; heart disease; renumatoid arthritis; renal; retinal; repertusion injury; immune disease; rheumatoid arthritis; renal; retinal; specific lupus erythematomysiis; enythema nodosum; myasthenia gravis; pernicious anaemia; dermatomyositis; enythema nodosum; myasthenia gravis; sporticious anaemia; dermatomyositis; enythema nodosum; myasthenia gravis; sporticious disorder; leukemia; sarcoma; myelonda; neuroma; melanoma; cancer; breast; colon; corrix; prostate; Hodgkin's disease; mon-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; spinal and an establication disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline. Streptokinase derived peptide 6 for amelioration of cell death. AAY25014 standard; peptide; 20 AA. 96US-0759599. 96US-0759599. 95US-0008233. (first entry) Krystal G, Rabkin SW; WPI; 1999-394231/33. RABK/) RABKIN S W. 3-DEC-1996; 06-DEC-1995; 05-DEC-1996; 23-AUG-1999 29-JUN-1999. US5917013-A. Synthetic. AAY25014; AAY25014 ID AAY 

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 7; Column 12; 15pp; English.

AMY25009-Y25019 are novel peptides derived from streptokinase that

ameliorate cell death. The products of the invention and their encoding

nucleic acids may be useful for treating diseases and conditions related

to aging, cellular differentiation, physical insult (e.g. physical

trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,

and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin

and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin

and any other organ), viral disorders (e.g. hepatitis, retroviral

infections, viral encephalitis, and AIDS/HIV), neurodegenerative

disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's

disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's

clerosis (FALS)), cardiovascular disease (e.g. atherosclerosis

myocardial infarction, heart failure, cardiomyopathy, myocardial

repertrusion injury, and hypertensive heart disease), immune disease (e.g.

repertrusion injury, and hypertensive heart disease), immune disease (e.g.

rheumatoid arthritis, systemic lupus erythematocous, insulin-dependent,
diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema

nodosum, Sjogrem's syndrome, temporal arthritis, myasthenia gravis,

Wegener's granulomatosis, glomerulonephitis, anti-phospholipid syndrome,
and autoimmune polyarthritides), a neopplastic disorder (e.g. leukemia,
arcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the

Claim 8; Column 5; 18pp; English.

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breast, brain, colon, cervix, and prostate, Hodgkin's disease and non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint disorders and inflammatory induced cell damage to the eye, brain and other organs), ischemia or reperfusion injury (e.g. myocardial ischemia and reperfusion injury, renal ischemia, spinal cord ischemia and/or insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other organs from chemicals, radiation, and other noxious substances), macular degeneration, cataract formation, and other noxious substances), macular ulcerative collisis, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord disease (e.g. motor and demyelinating disease), bypass surgery, chemotherapy, chemotherapy, chemically induced reperfusion, and therapeutics such as clozapine, AZT,
                                                                                                                                                                                                                                                                                                                                                                                                 and anthracyclines
            $$$$$$$$$$$$$$$$$$$
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20 AA; Sequence

Gaps ò 100.0%; Score 30; DB 20; Length 20; 100.0%; Pred. No. 2.4; 0; Indels 0; Mismatches 6; Conservative Query Match Best Local Similarity Matches 6; Conserv 1 SVDVEY 6 SVDVEY ઠે 셤

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ABB80006 standard; peptide; 20 AA. RESULT 6 **ABB8**0006

(first entry) 26-JUL-2002 ABB80006;

Streptokinase; cell death; apoptosis; necrosis; nootropic;
mutinflammatory; antidarkinsonian; anticonvulsant; cytostatic;
mutinflammatory; antidarkinsonian; anticonvulsant; cytostatic;
mutinflammatory; antidarkintic; antithematic; cardiant;
mutinfler; antidacterial; antidacerial; or perkinson; sisease; Mutington's disease;
matinlore; antidacerial; antidacerial; antidammatory disease;
matinlore; antidacerial; antidacerial; antidammatory disease;
matinlore; matinlore; antidammatory disease;
mycardial reperfusion injury; immune disease; autoimmune disease;
myclodegenerative diseases; viral diseases; macular degeneration;
myelodegenerative diseases; ulcerative colitis; pancreatitis; Streptokinase derived peptide#6. prion disease; aging 

Synthetic.

US6348567-B1

99US-0294457, 19-APR-1999; 19-FEB-2002.

95US-008233P. 06-DEC-1995; 05-DEC-1996; (MOLE-) MOLECULAR THERAPEUTICS INC.

Rabkin SW; Krystal G,

WPI; 2002-266542/31.

New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antiantentic, antiinchematic, cardiant, chematory, antiparkinsonian, anticonvulsant, cytostatic, antiantentic, antiincentic, anticipactic, immunosuppressive, anti-HIV, dermatological, antidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antianaemic, virucide, ophthalmological, antidiating peptides of the invention are useful for treating comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. parkinson's Alzheimer's Huntington's disease and cerebellar degeneration) neoplastic disorders including cancer, inflammatory disorders (e.g. nerthitis, inflammatory joint disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune systemic lupus erythematosus, diabetes mellitus, permicious anaemia), myolodegenerative diseases, viral diseases, and degenerative diseases, viral diseases, and degenerative diseases of any organ. Other disorders include macular degeneration, cataracts, conducederated aging. The current sequence represents a streptokinase of derived peptide of the invention with an ability to ameliorate cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             death in cardiac myocytes
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20 AA; Sequence

Gaps . 0 100.0%; Score 30; DB 23; Length 20; 100.0%; Pred. No. 2.4; ive 0; Mismatches 0; Indels Local Similarity 100 Query Match Best Loca Matches

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ABG76052 standard; peptide; 20 AA. RESULT 7 

ABG76052;

(first entry) 20-MAY-2003

Streptokinase fragment based, cell death ameliorating, 20mer peptide.

Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS; Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma; atherosclerosis; myocardial infarction; immune disease; cardinoma; rheumatoid arthritis; myocardial infarction; immune disease; cardinoma; rheumatoid arthritis; neoplastic disorder; inflammatory disorder; arthritis; inflammatory induced cell damage; motor neuron disease; physical insult; severe shock; ischaemia; reperfusion injury; cell death associated procedure; spinal cord reperfusion injury; toxic insult; liver toxicity, pulmonary toxicity; spinal cord disease; demotherapy; viral disease; viral encephalitis; infectious disease; bacterial disease; prion-based disease; macular degeneration; cataract formation; pancreatitis; Crohn's disease; ulcerative colitis; accelerated aging; oxidative stress.

Synthetic.

JS2002165129-A1.

07-NOV-2002.

31-JUL-2001;

95US-008233P. 99US-0294457. 06-DEC-1995; 19-APR-1999;

The invention relates to a pharmaceutical composition, which comprises a peptide capable of ameliozating cell death, its derivative or analogue, comprising a sequence Val-Asp-Val, where the peptide is in a suitable pharmaceutical camposition.

Comprising the peptide) is useful for treating or preventing cell death associated with a neurodegenerative disorder e.g. Parkinson's disease and Alzheimer's disease; cardiovaccular disease e.g. AIDS and therosclerosis and myocardial infarction; immune disease e.g. AIDS and therosclerosis and myocardial infarction; immune disease e.g. AIDS and inflammatory disorder e.g. arthritis and inflammatory induced cell damage; disease caused by physical insult e.g. trauma and severe shock; inflammatory disorder e.g. arthritis and inflammatory induced cell damage; disease caused by physical insult e.g. trauma and spinal cord control insult e.g. inver toxicity; and pulmonary toxicity; spinal cord disease e.g. motor neuron disease and duillain-Bare syndemic procedures associated with cell death e.g. bypass surgery and infectious disease e.g. hepatitis and viral encephalitis; crohn's disease; ulcertaive colitis; accelerated aging and oxidative stress in a warmblooded animal. The present sequence represents the amino acid sequence of a 20mer peptide capable of ameliorating cell death which is based on a construction or a capable of ameliorating cell death which is based on a Pharmaceutical composition for treating e.g. neurodegenerative disorder, cardiovascular disease, neoplastic disorder, viral disease and immune diseases, comprises a peptide capable of ameliorating cell Claim 2; Page 3; 19pp; English. 96US-0759599 Krystal G, Rabkin SW; WPI; 2003-246673/25 (KRYS/) KRYSTAL G. (RABK/) RABKIN S W. 05-DEC-1996; 

20 AA; Sequence

Gaps .. 100.0%; Score 30; DB 24; Length 20; 100.0%; Pred. No. 2.4; o; Mismatches 0; Indels 6; Conservative Local Similarity Query Match Matches

SVDVEY 6 1 SVDVEY 6

AAY25015 standard; peptide; 21 AA.

23-AUG-1999 (first entry) AAY25015;

Streptokinase derived peptide 7 for amelioration of cell death.

Streptokinase, cell death, amelioration, treatment; disease; aging; AlDS, cellular differentiation; physical insult; trauma; anoxia; hyperthermia, bypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; PALS; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; infarction; heart disease; cerebellar degeneration; cardiovascular disease; infarction; heart disease; cardiomyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lupus erythematosus; inalin-dependent, diabetes mellitus; pernicious anaemia; dermatomyositis; enthema nodosum; myasthenia gravis; Sjogren's syndrome; temporal arthritis; autoimmune polyarthitides; Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome; RESULT RAY25011 AAY25011 AAY25

melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; pancreatitis, Crohn's disease; ulcerative colitis; motor neuron disease; Guillan Bare Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline. neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;

Synthetic.

US5917013-A.

29-JUN-1999

96US-0759599 05-DEC-1996;

95US-0008233. 06-DEC-1995; 05-DEC-1996;

(RABK/) RABKIN S W.

Krystal G, Rabkin SW;

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 8; Column 12; 15pp; English.

AMY25009-Y25019 are novel peptides derived from streptokinase that ameliorate cell death. The products of the invention and their encoding nucleic acids may be useful for treating diseases and conditions related to conditions and their and their and their acids may be useful for treating diseases and conditions related to adding, cellular differentiation, physical insult (e.g. physical trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin cand any other organ), viral disorders (e.g. hepattis, retroviral infections, viral encephalitis, and AIDS/HIV), neurodegenerative disease, cerebellar degenerations, and familial amyotrophic lateral disease, cerebellar degenerations, and familial amyotrophic lateral sclerosis (FALS), cardiovascular disease (e.g. atherosclerosis, myocaddal linfarction, heart failure, cardiomyopathy, myocardial creption injury, and hypertensive heart disease), immune disease (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent, disbettes mellitus, lupus, perndcious anaemia, dermatconysit, savingment, temporal arthritis, mysthenia gravis, wegener's granulomatosis, glomerulomephritis, anti-phospholigid syndrome, and autoimmune polyarthritides), a necplastic disorder (e.g. lukemia, colon, cervix, and prostate, Hodgkin's disease and inflammatory induced cell damage to the eye, brain and other nodes and inflammatory induced cell damage to the eye, brain and other organs), ischemia or reperfusion injury (e.g. myocardial ischemia and or reperfusion injury, retinal ischemia or infarction, and stroke), toxic damage to other organs from chemicals, radiation, and other noxious substances, macular colon, cararact formation, panceatitis, Crohn's disease (e.g. undernative colitis, accelerated aging, spinal cord disease (e.g. myocardial section, and demonial suchemia and organican diseases, degeneration, cataract formation of the spinal cord disease (e.g. other organians) in and second surfary chanced encoder surfaract. Corgans and encodes surfary chanced encodes and diseas and demyelinating disease), bypass surgery, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT.

21 AA; Sequence

Gaps . 0 100.0%; Score 30; DB 20; Length 21; 100.0%; Pred. No. 2.6; ive 0; Mismatches 0; Indels 6; Conservative Local Similarity Query Match Matches

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1 SVDVEY 6

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SVDVEY

accelerated aging. The current sequence represents a streptokinase derived peptide of the invention with an ability to ameliorate cell

death in cardiac myocytes

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21

Sequence

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of cor its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, noctropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antiatherosalerotic, vasotropic, immunosuppressive, anti-HIV, dermatological, antidiabetic, antiatheamenic, virucide, ophthalmological, antidiabetic, antiparasitic. Peptides of the invention and entiparasitic. Peptides of the invention are useful for treating comprising peptides of the invention are useful for treating comprising peptides of the invention are useful for treating comprising peptides of the invention are useful for treating compressing of disease and cerebellar degeneration neoplastic disorders including cancer, inflammatory disorders (e.g. arthritis, inflammatory joint disorders), cardiovascular diseases (e.g. netritium, inflammatory joint cancer, inflammatory disorders (e.g. arthritis, inflammatory disorders diseases (e.g. arthritis, inflammatory dispasses), cardiovascular diseases (e.g. netriticious anaemia), confined immunodeficiency syntem diseases (e.g. netriticious anaemia), confined including macular degeneration, cataracts, and confined macular diseases, and diseases, and degenerative diseases, and degenerative diseases, and disease
                                                                                                                                                                                                                                                                                                     W neuroprotective; antiparking introducing interpretation; antinflammatory; antiparking anticonvulsant; overgiant;

A antiantencederotic; vasotropic; immunosuppressive; anti-HIV;

A dermatological; antidabetic; antinaamic; virucide; ophthalmological;

A mitialcer; antibacterial; antiparasitic; neurodegenerative disease;

A parkingon's disease; Alzheimer's disease; Huntington's disease;

A cerebellar degeneration; neoplastic disorder; cancer;

A inflammatory disorder; arthritis; inflammatory joint disorders;

A cardiovascular disease; heart failure; atherosclerosis;

M cardiovascular disease; heart failure; atherosclerosis;

M cardiovascular disease; heart failure; atherosclerosis;

M systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;

M myelodegenerative diseases; viral diseases; macular degeneration;

M cararact; Crohn's disease; ulcerative colitis; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders
                                                                                                                                                                                                                                                                                Streptokinase; cell death; apoptosis; necrosis; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR THERAPEUTICS INC.
                                                          ABB80007 standard; peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Column 5; 18pp; English
                                                                                                                                                                                                                         Streptokinase derived peptide#7.
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                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prion disease; aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-266542/31.
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                                                                                                                 ABB80007;
RESULT 9
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                         Gaps
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                                                                                                                                                                                                                               Antigenic peptide; streptokinase; streptokinase-specific antibody; thrombolytic activity; thrombolytic therapy; glomerulonephritis; rheumatic fever.
                                                                                                                                                                                                           Antigenic epitope of streptokinase, spanning amino acids 138-208
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 23; Length 21;
                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents an antigenic epitope of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 30; DB 20;
100.0%; Pred. No. 10;
ive 0; Mismatches 0;
DB 2
2.6;
                        Mismatches
Score 30;
Pred. No. 2
                                                                                                                                    AAY01550 standard; peptide; 71 AA.
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100.08;
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                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                   Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                            GEHO ) GEN HOSPITAL CORP.
           Local Similarity 100.
nes 6; Conservative
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les 6; Conserv
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                                                            1 SVDVEY 6
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                                                 1 SVDVEY
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 Query Match
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Matches
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RESULT 11 AAY01558

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induces fibrin-dependent plasmingen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of anno acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; a mucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proceolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold, The present represents recombinant streptokinase, designated rSK144-293.
                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated bacterial protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigenic peptide, streptokinase, streptokinase-specific antibody,
thrombolytic activity, thrombolytic therapy, glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide corresponding to amino acids 120-352 of streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 30; DB 20; Length 150; 100.0%; Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                            Claim 34; Page 67-68; 73pp; English.
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                                                                                                                                                                                                                                                                                                    N-terminally deleted streptokinase
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                                                               98WO-US26694
                                                                                                      97US-0069497
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                                                                                                                                                                                                                                   WPI; 1999-395183/33.
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Best Local Similarity
Matches 6, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatic fever
                                                               15-DEC-1998;
                                                                                                      15-DEC-1997;
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                        24-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a peptide corresponding to amino acids 148-293 of streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (PI) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. In is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus, streptokinase, fibrin-dependent plasminogen activator, nSK; rSK; bacterial; blood clot, thrombotic condition, myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                 ptide; streptokinase; streptokinase-specific antibody; activity; thrombolytic therapy; glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                        Peptide corresponding to amino acids 148-293 of streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides which bind streptokinase-specific antibodies useful in thrombolytic therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 13, 44pp; English.
AAY01558 standard; peptide; 146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY24796 standard; Protein; 150 AA.
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                                                                              (first entry)
                                                                                                                                                                                                                                                      Streptococcus equisimilis
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nes 6; Conservative
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                                                                                                                                                                   peptide;
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                                                                                                                                                                                                               rheumatic fever.
                                                                                                                                                                                       thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-1998;
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97US-0055911

18-AUG-1997;

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Streptokinase derivative having a C-terminal deletion (i.e. pro 373-bys 414) and Arg 45 to G19 68 also being deleted. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity.
The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction.
See also AAQ10230, AAR10195 and AAR10197-R10200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 348;
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                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 streptokinase; thrombolytic agent; myocardial infarction.
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                                           100.0%; Score 30; DB 100.0%; Pred. No. 52;
                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                           Streptokinase (1-372, 45-68 deficient)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SAKA ) OTSUKA PHARM FACTOR
                                                                                 6; Conservative
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                                                                                                                                                    183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-016179/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||||
SVDVEY 138
                                                            Best Local Similarity
Matches 6; Conserv
         297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                   1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-1990;
11-JUL-1989;
27-NOV-1989;
                                                                                                                                                                                                                                                                                                                       28-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP407942-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Majima E,
       Sequence
                                                                                                                                                                                                                                                                                   AAR10196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY24795
                                                                                                                                                                                                             RESULT 15
AAR10196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 16
AAY24795
ID AAY24'
XX
AC AAY24'
                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                  The present sequence represents a peptide corresponding to amino acids 120-352 of streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. Pl is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of streptokinase encoded by a pST-1 HindIII fragment. Recombinant streptokinase can be produced by culturing bacteria transformed with a high efficiency plasmid contg. the streptokinase gene, amplified by using haemolytic Streptococcus as the template and using inducers based on the streptokinase nucleotide sequence. The recombinant streptokinase is used to treat thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                streptokinase; recombinant production; haemolytic Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prepn. of streptokinase - useful for treating thrombus diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                         New polypeptides which bind streptokinase-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 30; DB 20; Length 233; 100.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR91599 standard; Protein; 297 AA.*
                                                                                                                                                                                  Disclosure, Page 13; 44pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 6-8; 24pp; Chinese
                                                                                                                                                useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYSH-) UNIV SHANGHAI MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-CN00024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94CN-0112106
                                                       Parhami-Seren B, Reed GL;
(GEHO ) GEN HOSPITAL CORP.
(HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                           WPI; 1999-190113/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-358628/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 SVDVEY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT29961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9527050-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-1994;
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AAR91599

RESULT 14

Song H;

Seguence Query Match ò

Gaps

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Truncated Met streptokinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Dawson KM, Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-208151/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 SVDVEY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ12159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVDVEY
                                                                                                                                                                                                                                                                                      07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                         07-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1990;
                                                                                                                                                                                                              409109125-A.
                                                                                                                                                                                                                                                   27-JUN-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR10195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR10195
 induces fibrin-dependent plasmingen activation in a pharmaceutical composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising a modified treptokinase protein; administering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminosen activator is useful for a bacterial fibrin-dependent plasminosen scrivator is useful for myocardial infarction, venous thrombosis. Pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified arterptokinase can also be used in non-human mammals. Streptokinase activation of plasminosen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least on amino acid substitution that inactivates a substrate site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present sequence represents recombinant streptokinase, designated rSK59-414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                  Streptococcus, streptokinase, fibrin-dependent plasminogen activator; nSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated bacterial protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 30; DB 20; Length 356; 100.0%; Pred. No. 64; ive 0; Mismatches 0; Indels (
                                   Recombinant streptokinase rSK59-414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 35; Page 65-66; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR12892 standard; Protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-terminally deleted streptokinase
                                                                                                                                                                                                                                                                                    98WO-US26694
                                                                                                                                                                                                                                                                                                                     97US-0069497
(first entry)
                                                                                                                                                          Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                        (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-395183/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 SVDVEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAXB0493
26-AUG-1999
                                                                                                                                                                                                                                                                                    15-DEC-1998;
                                                                                                                                                                                                                                                                                                                       15-DEC-1997;
                                                                                                                                                                                                              W09931247-A1
                                                                                                                                                                                                                                               24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
17-SEP-1991
                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR12892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Reed GL;
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Matches

ठ d RESULT 17 AAR12893

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Gapa
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ARCC 9642.

Minal and engineered to add a Met codon prior to codon 16 of the streptokinase CDS. The construct was used to prepare expression vector pGG06 for prodh. of the streptokinase core molecule.

See also AARL2887-R12889, AARL2891-R12893, AARL2885 and AARL3522. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
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Fusion protein, blood clotting, coagulation, fibrinolysis, antithrombotic, thrombolysis, streptokinase, thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         streptokinase; thrombolytic agent; myocardial infarction.
                                                                                           Streptococcus equisimilis ATCC 9542 or ATCC 10009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                2..369
/label= core streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptokinase (1-372, Phe 118 deleted).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 88; 115pp; English.
                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                             /note= "AAs 16-383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRBI-) BRITISH BIO-TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR10195 standard; Protein; 371 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              90WO-GB01911.
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Gaps

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Indels

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Length 372;

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256 and 257. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230, AAR10195-6 and AAR10198-R10200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lys 414) and retaining streptokinase activity. One or more of the amino acids can be replaced by a different amino acid at the same position or it can be deleted. Alternatively, an extra residue can be inserted into the sequence. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in platients with lung thrombus or myocardial infarction. See also AAQ10230 and AAR10195-R10199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                 streptokinase; thrombolytic agent; myocardial infarction
                                                                                                   , DB 12;
, 68;
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100.0%; Pred. No. 68;
iive 0; Mismatches 0;
                                                                                                                            0; Mismatches
                                                                                                   100.0%; Score 30; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakata Y,
                                                                                                                                                                                                                                             AAR10200 standard; Protein; 372 AA
                                                                                                                                                                                                                                                                                                                       Streptokinase (1-372) derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 59; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90JP-0096830.
89JP-0179432.
89JP-0307957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ono K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    90EP-0113099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAKA ) OTSUKA PHARM FACTOR
                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ogino K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-016179/03
                                                                                                                                                                             SVDVEY 162
                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 SVDVEY 162
                                                                            372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserv
                                                                                                                                                     1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AA;
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11-JUL-1989;
27-NOV-1989;
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                                                                                                                                                                                                                                                                                              28-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                  BP407942-A
                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Majima E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                              157
                                                                             Sequence
                                                                                                                                                                                                                                                                      AAR10200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                              Matches
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  8888888
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                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                  Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lys 414) and Phe at position 118 being deleted. Alternatively, Phe 118 can be replaced with any other amino acid. Derivatives show as decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230 and AAR10196-R10200.
                                                                                                                                        high purity prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lys 414) and Gln being substituted for Lys at both positions
                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                              Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  purity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptokinase; thrombolytic agent; myocardial infaction.
                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                        Uenoyama
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 30; DB 12; 100.0%; Pred. No. 67;
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                                                                                                                                        Synthetic gene encoding streptokinase - scale, of streptokinase used as a thrombolytic agent
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                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptokinase (1-372, Gln 256, Gln 257)
                                                                                      Sakata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR10197 standard; Protein; 372 AA
                                                                                                                                                                             Claim 8; Page 59; 76pp; English.
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89JP-0179432.
89JP-0307957.
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89JP-0179432.
89JP-0307957.
                                                                                      Ono K,
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                                                             (SAKA ) OTSUKA PHARM FACTOR
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es 6; Conservative
                                                                                      Ogino K,
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                                                                                                              WPI; 1991-016179/03
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                                                                                                                                                                                                                                                                                                                                                                                                                       156 SVDVEY 161
                                                                                                                                                                                                                                                                                                                                                                                               SVDVEY 6
                                                                                                                                                                                                                                                                                                                     371 AA
           11-APR-1990;
11-JUL-1989;
27-NOV-1989;
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11-JUL-1989;
27-NOV-1989;
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                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                      Мајіта Е,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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Gaps

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Indels

Length 372;

RESULT 21 AAY84006

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Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lya 414) and Pro residues being inserted next to Lya at both positions 256 and 257. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230, AAR10195-7 and AAR10199-R10200.
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Length 374;
                streptokinase; thrombolytic agent; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a mutant streptokinase.
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89JP-0179432.
89JP-0307957.
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                                                                                                                                                                                                                                                                       (SAKA ) OTSUKA PHARM FACTOR
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Best Local Similarity 100.
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Streptococcus
                                                                                                                                                              09-JUL-1990;
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                                                                                      EP407942-A.
                                                    Synthetic.
                                                                                                                                                                                                                                                                                                             Мајіта Е,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia Ojalvo A, De La Fuente Garcia JDJ;
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                                                                                                                                                              Amino acid sequence of a mutant streptokinase.
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                                                    AAY84006 standard; Protein; 372 AA
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                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                          Streptococcus equisimilis.
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Seralena Menendez A;
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                                                                                                                          03-JUL-2000
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                                                                                      AAY84006;
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RESULT 22
AAR10198
ID AAR10
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DT 28-MA
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DE Strep

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Gaps

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Gaps

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Indels

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Length 391;

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example of a streptokinase derivative which is a combination of two individually claimed modifications. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230, AAR10195-8 and AAR10200.
                                                                                                                                                                                                                                                                                                                                                                                            Streptokinase; SKC-2; plasminogen; plasmin; antigenicity; plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
                                                                                                                                     100.0%; Score 30; DB 12; 100.0%; Pred. No. 72;
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                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                     AAY84004 standard; Protein; 401 AA.
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                                                                                                                                                                                                                   134 SVDVEY 139
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                                                                                                            391 AA;
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Best Local S
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                                                        Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the Nor C-terminus -
                                                                                                                                             The present sequence represents a mutant protein of the streptokinase SKC-2. Streptokinase forms a complex with plasminogen, activating its conversion to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigenicity. The mutants are derived from the 1-1119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full-length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating myocardial infarction, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptokinase; thrombolytic agent; myocardial infarction.
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                                                                                                                        Disclosure, Page 24-25; 54pp; English
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89JP-0179432.
89JP-0307957.
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    Seralena Menendez A,
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                              2000-226041/20
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Matches 6; Conser
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                            WPI; 2000-226041,
N-PSDB; AAZ99252
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11-JUL-1989;
27-NOV-1989;
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Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
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De La Fuente Garcia JDJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complications and other forms of thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 18-20; 54pp; English.
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us-09-919-703-1.open.rag

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We streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; We cellular differentiation; physical insult; trauma; anoxia; hyperthermia; whypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; We hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; We wiral disorder; hepatitis; retroviral; infection; encephalitis; FALS; heart disease; cerebellar degeneration; cardiovascular disease; Mintaington's disease; cardiovascular disease; Alaxieimer's disease; Mintaington's disease; cardiownopathy; hypertenaive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; we perfusion injury; immune disease; rheumatoid arthritis; renal; retinal; we systemic lupus erychematosus; insulin-dependent; diabetes mallitus; pernicious anaemia; dermatomyositis; enythema nodosum; myasthenia gravis; Sogren's syndrome; temporal arthritis; autoimmune polyarthritides; wegener's granulomatosis; glomerulomephritis; anti-phospholiphi gyrdion; spinal concer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's Lymphoma; inflammatory disorder; stroke; ischemia; melanoma; cancer; toxic insult; pulmonary; macular degeneration; cataract; perical concer; toxic insult; pulmonary; macular degeneration; cataract; chercal concer; cataract; 
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                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation
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                                                                             Indels
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                              Pred. No. 74;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY25020 standard; peptide; 413 AA
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0008233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                             6; Conservative
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                                                                                                                                                                                                                                       144 SVDVEY 149
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                                  Best Local Similarity
                                                                                                                                                      1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-1999
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                                                                             Matches
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AAY25,020

AAY25,020

XX XX XA AAY2

XX XA AAY2

XX XX Early Flam, bypool of the family fla
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reperfusion injury, and hypertensive heart disease), immune disease (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent, diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema nodosum, Sjogrem's syndrome, temporal arthritis, mysathenia gravis, Negener's granulomatosis, glomerulomephritis, anti-phospholipid syndrome, and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia, sarcomas, myslomas, carcinomas, melanoma, cancers of the breast, brain, colon, cervix, and prostate, Hodgkin's disease and non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint disorders and inflammatory induced cell damage to the eye, brain and other organs), ischemia or reperfusion injury, renal ischemia, spinal cord ischemia and/or reperfusion injury, reinal ischemia, spinal cord ischemia and/or reperfusion injury, reinal ischemia, spinal cord ischemia and/or result (e.g. liver toxicity, pulmonary toxicity, toxic damage to other organs from chemicals, radiation, and other noxicus substances), macular degeneration, cataract formation, pancreatitis, crohn's disease, ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor neuron disease, bypass surgery, chemotherapy, and empeliation demonstration of the spinal cord, Guillan Bare Syndrome chemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                       chemically-induced reperfusion, and therapeutics such as clozapine, AZT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a mutant protein of the streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garcia Ojalvo A, De La Fuente Garcia JDJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptokinase, SKC-2; plasminogen, plasmin; antigenicity, plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 30; DB 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a mutant streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY84005 standard; Protein; 413 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Torrens Madrazo IDC,
Seralena Menendez A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-226041/20
                                                                                                                                                                                                                                                                                                                                                                                                             and anthracyclines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 SVDVEY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY84005;
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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, noctropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, antiparkinsonian, anticonvulsant, cytostatic, antiartherosaleterotic, vasotropic, immunosuppressive, anti-HIV.

CC antialfarerosaleterotic, vasotropic, immunosuppressive, anti-HIV.

CC dermatological, antidiabetic, antianaemic, virucide, ophthalmological, antiulcer, antibaressitic. Peptides of the invention are useful for treating comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. harkinson's, Alzheimer's, Huntington's comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. harkinson's, Alzheimer's, Huntington's cancer, inflammatory disorders (e.g. arthritis, inflammatory joint disorders), cardiovascular diseases (e.g. heart fallure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune diseases, acquired immunodeficiency syndrome (AlDS), rheumatorial arthritis, systemic lupus erythematosus, diabetes mellitus, pernicious anaemia), myelodegenerative diseases, viral diseases, and degenerative diseases, viral diseases, and degeneratics, infectious diseases including bacteria, parasite, prion-based diseases, and eryancher sanding reperent sequence represents a representative

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Contractions of the contraction 
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SKC-2. Streptokinase forms a complex with plasminogen, activating its conversion to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigenicity. The mutants are derived from the 1-119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating myocardial inflatorion, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
0
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 21; Length 413; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cataract; Crohn's disease; ulcerative colitis; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80012 standard; protein; 413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptokinase amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Query Match
Best Local Similarity 100.00
Best Local Similarity 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prion disease; aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 SVDVEY 149
                                                                                                                                                                                                                                                                                                                                                  Sequence 413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB80012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 28
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100.0%; Score 30; DB 23; Length 413; 100.0%; Pred. No. 76;

streptokinase amino acid sequence.

413 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156..171
/label= 18mer_peptide
/note= "Cell death amelloxating peptide. Specifically
claimed in claim 2. This is SEQ ID NO 5 as shown
in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
156..161
/label= Gmer_peptide #1
/note= "Cell death ameliorating peptide. Specifically
claimed in claim 2"
                                                                                                 Gaps
                                                                                            Ö
                                                                                        0; Indels
                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Representative streptokinase sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     accelerated aging; oxidative stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG74199 standard; Protein; 413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2003 (first entry)
Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                       156 SVDVBY 161
                                                                                                                                                                   1 SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                        RESULT 29
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New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

Disclosure, Fig 3, 18pp, English

(MOLE-) MOLECULAR THERAPEUTICS INC

Krystal G, Rabkin SW;

WPI; 2002-266542/31.

99US-0294457. 95US-008233P.

9-APR-1999; 06-DEC-1995; 05-DEC-1996;

19-FEB-2002.

/note= "Cell death ameliorating peptide. Specifically claimed in claim 2. This is SEQ ID NO 5 as shown on page 8".

156..176 /label= Fraction\_13\_peptide /note= "Cell death ameliorating peptide. Specifically claimed in claim 2"

6mer peptide #2
'Cell death ameliorating peptide. Specifically
claimed in claim 2"

/label= 6mer\_peptide\_ /note= "Cell\_death\_am\_

309

//abel= 11mer\_peptide
/note= "Cell death ameliorating peptide. Specifically
claimed in claim 2"

/label= Fraction 12 peptide /note= "Cell death ameliorating peptide. Specifically claimed in claim 2"

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31-JUL-2001; 2001US-0919703
                                                                                  Krystal G, Rabkin SW;
                                                                                       WPI; 2003-246673/25.
                                                                          (KRYS/) KRYSTAL G.
(RABK/) RABKIN S W.
                                                  JS2002165129-A1.
                                                                 06-DEC-1995;
                                                                   19-APR-1999;
05-DEC-1996;
                                                                                                                                                                        Sequence
                                     Peptide
                 Peptide
                           Peptide
       Peptide
                                                                                                    death
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of streptokinase used as a thrombolytic agent
                                                                                                                                                                                Ono K, Sakata Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 51; 76pp; English.
                                                                                                              (SAKA ) OTSUKA PHARM FACTOR
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(first entry)
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                                                                                                                                                                                Majima E, Ogino K,
                                                                                                                                                                                                                                                  WPI; 1991-016179/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 AA;
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21-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a pharmaceutical composition, which comprises a peptide capable of ameliorating cell death, its derivative or analogue, comprissing a sequence Val-Aspe-Val, where the peptide is in a suitable pharmaceutical composition a suitable pharmaceutical composition comprising the peptide) is useful for treating or preventing cell death associated with a neurodegenerative disorder e.g. Parkinson's disease and Alzheimer's disease; cardiovascular disease e.g. AIDS and atherosclerosis and myocardial infarction; immune disease e.g. AIDS and inflammatory disorder e.g. arthritis morphastic disorders e.g. leukaemia and carcinoma; inflammatory disease caused by physical insult e.g. trauma and severe shock; ischaemia or reperfusion injury e.g. myocardial ischaemia and spinal cord capacitation injury e.g. myocardial ischaemia and spinal cord capacitation injury e.g. myocardial ischaemia and spinal cord disease e.g. nepatitis and viral encephalitis; conclusively viral disease e.g. nepatitis and viral encephalitis; infectious diseases e.g. hepatitis and viral encephalitis; or infectious diseases e.g. hepatitis and viral encephalitis; or infectious diseases e.g. hepatitis and viral encephalitis; or infectious diseases e.g. hepatitis encephalitis; crohr's disease; blooded animal. The present sequence represents the amino acid sequence of a representative streptokinase from which the cell death ameliorating peptides are produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                Pharmaceutical composition for treating e.g. neurodegenerative disorder, cardiovascular disease, neoplastic disorder, viral disease and immune diseases, comprises a peptide capable of ameliorating cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3; 19pp; English
95US-008233P.
99US-0294457.
96US-0759599.
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic gene encoding streptokinase - scale, high purity prodn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 100.0%; Score 30; DB 12; Length 414; Local Similarity 100.0%; Pred. No. 76; Osservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptokinase and its derivatives can be produced in large quantities with high purity for use as thrombolytic agents patients with lung thrombus or myocardial infarction. See also AAR10195-R10200.
                                                                                                                                                                streptokinase; thrombolytic agent; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasminogen activator; coronary thrombosis; ATCC-9542
                                                                                                                                                                                                                                                                                                                                         Uenoyama
                                                                                                                                         Streptokinase encoded by synthetic gene.
                                                                         AAR10194 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                        90JP-0096830.
89JP-0179432.
89JP-0307957.
                                                                                                                                                                                                                                                     90EP-0113099.
                     156 SVDVEY 161
 1 SVDVEY
                                                                                                                    28-MAR-1991
                                                                                                                                                                                                                                                    09-JUL-1990;
                                                                                                                                                                                                                                                                         11-APR-1990;
                                                                                                                                                                                                                                                                                    11-JUL-1989;
                                                                                                                                                                                                                                                                                             27-NOV-1989;
                                                                                                                                                                                                                               16-JAN-1991
                                                                                                                                                                                                         EP407942-A.
                                                                                                                                                                                    Synthetic.
                                                                                               AAR10194;
                                                               AAR10194
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Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                             14-414 of streptokinase, which binds to plasminogen and does not have a sequence comprising amino acids 60-414 is new. The polypeptide pref. comprises amino acids 244-352, 1-352, 120-352 or 244-414.
                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 30; DB 15; Length 414; larity 100.0%; Pred. No. 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                   DNA encoding a polypeptide which binds to plasminogen and corresponds to region of streptokinase - useful to detect plasminogen in a sample and to treat myocardial infarction
                                                                                                                                                                                                                                                                                                  Nucleic acid comprising a sequence encoding amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus equisimilis native streptokinase.
                                                                                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                  Disclosure; Page 40-41; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 30; Page 60-61; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY24794 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminally deleted streptokinase
                                          92US-0956692,
             93WO-US09502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US26694
                                                                                        (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus equisimilis
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                                                                                                                                                                   WPI; 1994-135561/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVDVEY 6
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                                          05-OCT-1992;
29-SEP-1993;
             05-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                        Reed GL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                               Streptokinase C-2 gene from S.equisimilis type C - plasmids and transformants for large scale intra- and extracellular expression of SKC-2 useful in thrombolytic agents
                                                                                                                                        Hidalgo AP, Doce RS, Marrero LFH;
Munoz EAM, Martinez WB, Somavilla MC;
Martinez LSH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 30; DB 13; Length 414; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptokinase; SK; Streptococcus equisimilis; plasminogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                       (INGG-) CENT ING GENETICA & BIOTECNOLOGIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14..414
/note= "claim 1, see
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244..414
/note= "claim 3,
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                                                                                                                                                                                                                                                                                                                  Claim 13; Page 14; 28pp; English
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                                             91AU-0078101.
                                                                           90CU-0000090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.00
Best Local Similarity 6; Conservative
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16-NOV-1994' (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus equisimilis
                                                                                                                                        Chaplen RR,
Ramirez AC,
                                                                                                                                                                        Garcia J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120..352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myocardial infarction.
                                                                                                                                                                                                    WPI; 1992-024716/04.
N-PSDB; AAQ20665.
                                                                                                                                                                                                                                                                                                                                                                                                                                               and a T4 terminator.
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| SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 AA;
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                                                                                                                                                                        Fernandez AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptokinase
                                                                                                                                        Garcia MPE,
                                             31-MAY-1991;
                                                                             23-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9407992-A1
              28-NOV-1991
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                                                                                                                                                        Collazo PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157
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RESULT 32

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Gaps

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describes a synthetic polypeptide (PI) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. PI is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic

414 AA

Sequence

888888

us-09-919-703-1.open.rag

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The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising can mucleic acid (1) encoding a modified bacterial streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an carbor comprising (1); and (4) a host cell transformed with the expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising (2) and bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in parients with a thrombosis. The modified confiction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified attention of plasminogen is at least to fold, preferably 100-fold grader in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least to fold, preferably 100-fold carboridates a substrate site for proteolytic cleavage. This reduces the interpresents native streptokinase at least two-fold. The present control protein that the presents native streptokinase at least two-fold. The present control protein at least to the control presents at least to the control present the present control presents at least two-fold. The present control presents at least two-fold. The present control presents at least two folds. The present control presents at l
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thrombolytic activity; thrombolytic therapy; glomerulonephritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides which bind streptokinase-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a native streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY01556 standard; peptide; 414 AA.
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| SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                  Gaps
                                                                                                                                                                                                                                                                                                       Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic; plasma clot, hydrolysis; haemolytic Streptococcus; plasminogen; plasmin; serine protease; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant streptokinase polypeptide - useful as plasmin-resistant
 100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76;
                                  Indels
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                                                                                                                                                                                                                                                                           Streptococcus equisimilis native streptokinase.
                                  0; Mismatches
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                                                                                                                                                                             AAW94664 standard; Protein; 414 AA.
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                                                                                                                                                                                                                                                                                                                                                                        fibrinolysis; resistance.
                                    6; Conservative
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                                                                                                157 SVDVEY 162
Query Match
Best Local Similarity
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                                                                   1 SVDVEY 6
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                                                                                                                                                                                                             AAW94664;
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                                     Matches
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Non-immunogenic, epitope, T-cell, immunogenicity; immune system; SK; immunogl bulin; therapeutic; streptokinase.

Streptococcus equisimilis.

W09852976-A1

26-NOV-1998

98GB-0007751. 97GB-0010480. 97GB-0016197. 97GB-0025270. 97US-0067235.

(BIOV-) BIOVATION LTD.

Carr FJ;

28-NOV-1997; 02-DEC-1997;

21-MAY-1997;

31-JUL-1997

98WO-GB01473

21-MAY-1998;

Streptokinase (SK) protein sequence

AAW86143 standard; Protein; 414 AA.

AAW86143 RESULT

AAW86143;

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                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin; serine protease; fibrin; blood clot; thrombolytic; vascular thromboembolytic symptom; acute myocardial infarction;
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Length 414;
                                                                   Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus equisimilis mutant streptokinase K59E.
   DB 20;
   100.0%; Score 30; DB
100.0%; Pred. No. 76;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                        Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                      157 SVDVEY 162
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          Query Match
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The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein; (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immunogenicity of the protein when exposed to the immune or system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of the SK protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
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100.0%; Score 30; DB 20; Length 414;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW86144 standard; Protein; 414 AA.
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AAW86144
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AC AAW8
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Gaps

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Best Local Similarity 100. Matches 6; Conservative

157 SVDVEY 162

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1 SVDVEY

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EP1024192-A2

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The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein, (b) identifying in the amino acid sequence or or more potential epitopes for T-cells (T-cells epitopes) of the given species, and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of a de-immunised SK protein molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy; cardiovascular disorder; fibronectin.
                                         Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunogl bulin; therapeutic; streptokinase; de-immunised.
                                                                                                                                                                                                                                                                                                                                                                                                          proteins - by modifying the amino acid eliminate potential epitopes for T-cells
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             De-immunised streptokinase (SK) protein sequence
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97GB-0016197.
97GB-0025270.
97US-0067235.
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les 6; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                            Reducing immunogenicity of sequence of the protein to of a given species
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                                                                                          Streptococcus equisimilis
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31-JUL-1997;
28-NOV-1997;
02-DEC-1997;
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                                                                                                                         W09852976-A1
                                                                                                                                                                                        21-MAY-1998;
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                                                                                                                                                        26-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                 Carr FJ;
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This sequence represents the human Streptococcus equisimilus streptokinase protein sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between plasminogen activator (PA) comprises a polypeptide fusion between attreptokinase (SX) which are capable of plasminogen (PG) activation, and fibrin binding regions of human fibronectin, which are from fibrin and fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable command or human PG. The hybrid streptokinase-fibrin binding domain polypeptides are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as conditional as kinetics of plasminogen activation that are distinct from that of natural streptokinase in the natural rate of the catalytic conversion of plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after controlating blood plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after controlating blood plasmin con plasmin, thus adding in the circulating blood plasminogen activation process to the site of paranilaginal thrombus. This overcomes systemic plasminogen activation centuatered during clinical use of streptokinase.
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of
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                                                                                                                                                                Sahni G, Kumar R, Roy C, Rajogopal K, Nihalani D, Sundaram V;
Yadav M;
                                                                                                                                                                                                                                                                                              Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Similarity 100.0%; Score 30; DB 21; Length 414;
6; Conservative 0; Mismatchee n. ---
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                                                                                                                                               (COUL ) CSIR COUNCIL SCI IND RES
                                                                                                                                                                                                                                                                                                                                                                             Sxample 3; Fig 3; 58pp; English
                                                                         99EP-0310541
                                                                                                          98IN-0003825
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                                                                                                                                                                                                                                          WPI; 2000-516032/47.
N-PSDB; AAA37633.
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Best Local Similarity
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                                                                         3-DEC-1999;
                                                                                                              24-DEC-1998;
                                    02-AUG-2000.
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Gaps

The second secon

plasmin; myocardial infarction

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Exproteins or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at least one of these T cell cepitopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for the producing a protein with an enzymatic activity which has a beneficial ceffect, a protein used to convert inactive days to its active form within a living organism, a vaccine, a protein used as a carrier of other molecule or a protein which binds to other molecules within or introduced within the living organism. The less immunogenic bio distribution of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic correction is useful in medicine, diagnosis and in manufacture of a protein is useful in medicine, diagnosis and in manufacture of a certain strains of beta-haemolytic streptokinase is produced by certain strains of beta-haemolytic streptokinase is produced by certain strains of beta-haemolytic streptokinase is produced by protein tain its activation to plasmin and thereby promoting the corentation of fibrin filaments in blood clots. Streptokinase is an effective thrombolytic agent in the treatment of coronary thrombosis, my morein to a single use. The new method could provide a longer coronary and preserving left ventricular function following protein to a single use. The new method could provide a longer therapeutic use for streptokinase. This is the sequence of the wild type streptokinase. The altered streptokinase sequence is given in AAB01296. See GENESEQ records AAB01289-801302.
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                                                                                                                                                                                                                                                                                                    Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Altered streptokinase from Streptococcus equisimilis.
                                                                                                                                                                                                                        Carr FJ, Adair FS, Hamilton AA, Carter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB01296 standard; protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 5; 42pp; English
                                                                             99WO-GB04119
                                                                                                                      98GB-0026925
                                                                                                                                           99GB-0002139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVDVEY
WO200034317-A2
                                                                               38-DEC-1999;
                                                                                                                        38-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2000
                                                                                                                                             02-FEB-1999;
                                        15-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB01296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB01296
ID AAB0
XX
XX
XX
DT 25-5
XX
DE Alte
XX
KW Imm
KW vach
KW pla
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rectains or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at least one of these T cell epitopes to reduce the immunogenicity of the protein when exposed to epitopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for producing a protein with an enzymatic activity which has a beneficial therapeutic effect, a protein used to convert inactive drugs to its active form within a living organism; a vaccine, a protein used as a carrier of other molecules or a protein which binds to other molecules within or introduced within the living organism; in order to alter the bio distribution of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic protein is useful in medicine, diagnosis and in manufacture of a certain strains of beta-haemolytic streptoxinase is produced by certain strains of beta-haemolytic streptoxinase is produced by contract or its ability to efficiently bind human plasminogen, or inherent enzymatic activity but has considerable clinical importance contraction of fibrin filaments in blood clots. Streptokinase is an effective thrombolytic agent in the treatment of coronary thrombosis, effective thrombolytic agent in the reatment of coronary thrombosis, improving survival and preserving left ventricular function following mycoardial infarction. The new method could provide a longer protein to a single use. The new method could provide a longer the ratered streptoxinase. This is the sequence of the altered streptoxinase. This is the sequence is given in AAB01295. See GENESEQ records AAB01289-B01302.
                                                                                                                                                                                                                                                                                                                                                                                       Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 30; DB 21; Length 414; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                Hamilton AA, Carter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB74940 standard; Protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sxample 2; Fig 6; 42pp; English.
                                                                                                                                                                                                            98GB-0026925.
99GB-0002139.
                                                                                                                                                                       99WO-GB04119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001 (first entry)
                                                   Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                         (BIOV-) BIOVATION LTD.
                                                                                                                                                                                                                                                                                                                Carr FJ, Adair FS,
                                                                                                                                                                                                                                                                                                                                                    4PI; 2000-423372/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||||
157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVDVEY 6
                                                                                           40200034317-A2
                                                                                                                                                                                                                08-DEC-1998;
                                                                                                                                                                         38-DEC-1999;
                                                                                                                                                                                                                                      02-FEB-1999;
                                                                                                                                  15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB74940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 42
AAB74940
ID AAB74,
XX
AC AAB74,
DT 02-JU
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Mutant streptokinase protein sequence K59E.
                                               Wu H, Shr G;
                                     11-JUL-1995;
                                        11-JUL-1995;
       Unidentified
                                  01-JAN-2001.
                              TW416990-A.
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Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                           Streptococcus plasminogen activator, streptokinase
                                                                                              Plasminogen activator, cardiant, thrombolytic;
heart attack; stroke; blood clotting disorder.
                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 29-31; 41pp; English.
                                                                                                                                                                                                                              (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                 AAY99593 standard; protein; 415 AA.
                                                                                                                                                                                         16660SD-0M66
                                                                                                                                                                                                                                                 Zhang XC, Tang JJN
                                                        (first entry)
                                                                                                                                                                                                                                                                    WPI; 2000-422975/36.
                                                                                                                               Streptococcus sp.
                                                                                                                                                WO200032759-A1.
                                                                                                                                                                                         06-MAY-1999;
                                                                                                                                                                                                            02-DEC-1998;
                                                                                                                                                                     38-JUN-2000.
                                                                                                                                                                                                                                                                                                                        plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                      AAY99593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                   Lin X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
RESULT 43
        AAY99593
ID AAY
                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                   Preparation of novel streptokinase mutants as improved thrombolytic
                                                                                                                              /label= unknown
/note= "given as being encoded by NNN due to poor
quality text"
         Streptokinase; mutant; human; plasmin; plasminogen; thrombolytic.
                                                                                                /note= "given as being encoded by NNN due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 30; DB 22; Length 414; 100.0%; Pred. No. 76; cive 0; Mismatches 0; Indels
                                                                     'note= "Lys in wild type sequence
                                                                                                            quality text
                                                Location/Qualifiers
                                                                                         /label= unknown
                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1; 4pp; Chinese.
                                                                                                                                                                                                                                 95TW-0107238.
                                                                                                                                                                                                              95TW-0107238
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Matches 6; Conservative
                                                                                                                                                                                                                                                  (NASC-) NAT SCI COUNCIL
                                                                                                                                                                                                                                                                                           WPI; 2001-326604/34.
                                                                                                                      Misc-difference 370
                                                                                Misc-difference 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 AA
                                                                                                                                                                                                                                                                                                    N-PSDB; AAF82144
                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The present sequence is streptokinase, a single-peptide secretory protein which is produced by various strains of haemolytic Streptococcus. Streptokinase forms a tight binding complex with human plasminogen, causing the spontaneous conversion of plasminogen to its active form, plasminogen is the principal serine protease zymogen in the extracellular fluids of vertebrates. Plasminogen is implicated in perioellular proteolysis associated with a wide range of physiological processes. Plasminogen activators regulate plasminogen expression either by forming a binding complex, as in the case of streptokinase, or by hydrolysing a peptide bond in plasminogen to convert it to plasmin. Review of sequence homologies of several plasminogen activators and chymotrypain has identified a six amino acid peptide involved in plasminogen activation. This peptide is particularly useful the inserted between maino acid residues 644 and 645 of full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human plasminogen. Novel plasminogen activators have been made based upon the plasminogen activation/recognition site of plasminogen binding proteins. The polypeptides are useful in preparing thrombolytic agents for treating blood clotting disorders such as heart attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 30; DB 21; Length 415; 100.0%; Pred. No. 77; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY50870 standard; protein; 415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY50870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 44
AAYSO870
ID AAYSOX
XX
AC AAYSOX
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Gaps

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1 SVDVEY 6

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SVDVEY

us-09-919-703-1.open.rag

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Streptokinase produced using E.coli transformed with a recombinant streptokinase vector can be isolated for use as a thrombolytic agent to facilitate the in vivo lysis or dissolution of blood clots. The vector is esp. a plasmid obtd. From E.coli, esp. plasmid pBR 322. Recombinant plasmid pMF1 as defined by a restriction endonuclease map is claimed. Escherichia coli HB 101 harbouring plasmid pMF1 is depositd as ATCC 39613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptokinase A; recombinant phage; thrombolytic agent; plasminogen; plasmin.
                                                                                                                                                                                                                                                                                                                        - by cultivating Escherichia coli ATCC 39613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High yield streptokinase A prodn. from infected bacteria - contg. recombinant phage including gene from Streptococcus, useful as thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptokinase A from Streptococcus pyogenes SF130/13
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0
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llarity 100.0%; Pred. No. 82;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR06378 standard; protein; 440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DEAK ) AKAD WISSENSCHAFTEN DDR.
                                                                                                                                                                                                                                                                                                                                Streptokinase prodn. – by culti
contg. recombinant plasmid pMF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 2, 7pp, German
                                                                                                                       PHILLIPS PETROLEUM CO. UNIV OF OKLAHOMA.
                                                                                                                                                                                                                                                                                                                                                                                                             Example, Fig 2; 28pp; English.
               84US-0585417.
83DD-025553.
83DD-0255235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88DD-0321532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88DD-0321532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
                                                                                                                                                                                                 Malke H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walter F, Siegel M,
                                                                                                                                                                                                                                                   WPI; 1985-135032/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-247328/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ05604.
                                                                                                                                                                                                                                                                              N-PSDB; AAN50493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SVDVEY
                     02-MAR-1984;
10-OCT-1983;
10-OCT-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1988;
                                                                                                                                                                                                   Ferretti JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
20-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD276694-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR06378;
                                                                                                                       (PHIP ) 1
(UYOK-) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query, Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel thrombolytic agent comprising streptokinase where at least one nonessential portion has been modified. The invention also describes a method of forming a thrombolytic agent comprising determining a nonessential portion of streptokinase and modifying the nonessential portion to render the resulting protein less antigenic. The modified streptokinase is used to treat blood clot disorders, such as heart attacks. The modified streptokinase has less antigenicity than streptokinase but is still able to complex plasminogen and lead to plasminogen activation. Modified streptokinase with the nonessential portions removed or trundated simplify the molecule. Such smaller proteins are cheaper and easier to produce. This sequence represents a fragment of a Streptococcus sp. streptokinase protein which is used in the description of the method of the invention.
                                                                                               Thrombolytic agent; streptokinase; antigenic; blood clot; heart attack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New thrombolytic agents derived from modified humanized streptokinase, useful for treating blood clot disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 30; DB 21; Length 415; 100.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoded by skc streptokinase gene on the 2.5kb PstI
produced pMF1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ົວ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·
0
                                               Streptococcus sp. streptokinase protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzyme; thrombolytic agent; blood clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 48-49; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                     (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP50620 standard; Protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                   99WO-US10086
                                                                                                                                                                                                                                                                                                                                                                                     98US-0084392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin X, Tang JJN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84AU-0033859
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-052966/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVDVEY
                                                                                                                                                                                                                              W09957251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-1984;
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                     06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-1991
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9
                                                                                                                                                                                                                                                                                   11-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang XC,
                                                                                                                               treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP50620;
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IID AAP5

AAC AAP5

XXX I 16-0

XXX Sequence prod

XXX Enzy

YXX Enzy

YX E
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Gaps

; 0

Gaps

.. 0

Indels

ö 11;

100.0%; Score 30; DB 100.0%; Pred. No. 82; ive 0; Mismatches

Conservative

9

Length 440;

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Query Match
Best Local Similarity
Matches 6; Conserv
                                         1 SVDVEY
                                                                                                                                        AAR12889;
                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                      Protein
                                                                                              RESULT 48
                                                                                                         AAR12889
                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid pWM1 (contg. the streptokinase G gene ) is ligated with pUC19 and the resultant product used to transform bacteria. Infected cells are cultured in lig. medium contg. assimilable C and N sources, and streptokinase G is isolated from the cell lysate.

The infected cells provide the protein in high yields, i.e. 600 U/ml which is 1.5-2 times that for the donor strain.

The protein activates the autocatalytic conversion of human plasmin, so is potentially useful as a thronbolytic agent. See also DD-276694 (AAQ05604).

(Updated on 25-MAR-2003 to correct PA field.)
           Lambda L47.1 is ligated with genomic DNA from S. pyogenes SF130/13 and the resultant product used to transform bacteria. Infected cells are cultured in liq. medium contg. assimilable C and N sources, and streptokinase A is isolated from the cell lysate. The infected cells provide the protein in high yields, i.e. 1000 U/ml compared to 80 U/m; for the donor strain. The protein activates the autocatalytic conversion of human plasmin, so is potentially useful as a thronbolytic agent. See also DD-276693 (AAQ05603).
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High yield streptokinase G prodn. from recombinant cells -
transformed with plasmid contg. gene from Streptococcus, useful
                                                                                                                                                                         0,
                                                                                                                                      In 100.0%; Score 30; DB 11; Length 440; Similarity 100.0%; Pred. No. 82; 6; Conservative 0; Mismarchor
                                                                                                                                                                                                                                                                                                                                               Streptokinase G protein from Streptococcus pyogenes G19908.
                                                                                                                                                                                                                                                                                                                                                                     Streptokinase G; thrombolytic agent; plasminogen; plasmin;
                                                                                                        (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                        AAR06377 standard; protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DEAK ) AKAD WISSENSCHAFTEN DDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walter F, Siegel M, Malke H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88DD-0321531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88DD-0321531
                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-247327/33.
                                                                                                                                                                                                             183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                  recombinant plasmid
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 AA;
                                                                                                                                  440 AA;
                                                                                                                                                                                              1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ05603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1988;
                                                                                                                                                                                                                                                                                                                  25-MAR-2003
20-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                           DD276693-A.
                                                                                                                                                                                                                                                                                               AAR06377;
                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                     RESULT 47
                                                                                                                                                                                                                                                                g
     8
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The sequence was deduced from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C ) ATCC 10009 or ATCC 9642. The primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]). See Swiss-Prot K02986 and P00779 and Geneseq N70106. The gene can be used to construct expression ecrocis in which the streptokinase gene is linked to a second gene encoding e.g. another streptokinase protein, hirudin, or a streptokinase-like protein, via a linking sequence encoding a cleavage kinase-like protein, via a linking sequence encoding a cleavage fusion protein are present at the site of the target thrombus so the active agents are released specifically at the place where clot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                     blood clotting; coagulation; fibrinolysis; thrombolysis; streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n is occurring.
R12887, R12888, R12891-R12894, R12885 and R12522
on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equisimilis ATCC 9542 or ATCC 100009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27..440
/label= mature streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB
Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...26
'label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 80; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                           AAR12889 standard; Protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRBI-) BRITISH BIO-TECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
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89GB-0027722
                                                                                                                                                                                                                                                  (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dawson KM, Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-208151/28
183 SVDVEY 188
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ12156
                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein;
antithrombotic;
                                                                                                                                                                                                                                                                                                                                       Streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Formation is
                                                                                                                                                                                                                                                  25-MAR-2003
17-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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||||||| 183 SVDVEY 188

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AAR12885 standard; Protein; 483 AA.
                                       RESULT 50
AAR12885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antinilammatory activity. [1], nucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by creptococcus bacteria, particularly S. agalactica and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a composition comprising (1) or a nucleic acid encoding (1), may be consequently a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be maningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be cused in gene therapy. Antibodies to (1) are used for affinity changing antipococcus proteins.
ö
                                                                                                                                                                                Streptococcus, GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus, Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
 Gaps
 .
0
 Indels
                                                                                                                                                                                                                                                                                                                                                                                          Masignani V, Margarit Ros YI, Grandi G,
 ;
0
 Mismatches
                                                                                                                                                            Streptococcus polypeptide SEQ ID NO 8298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 3946; 4525pp; English.
                                                                                                 ABP29561 standard; Protein; 440 AA
  ..
                                                                                                                                                                                                                                                                                                                  27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                              29-OCT-2001; 2001WO-GB04789
                                                                                                                                           02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                             (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
  6; Conservative
                                                                                                                                                                                                                                 Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-352536/38.
N-PSDB; ABN70192.
                                           183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 AA
                       1 SVDVEY 6
                                                                                                                                                                                                                                                      WO200234771-A2.
                                                                                                                                                                                                                                                                           02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                             Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                       ABP29561;
   Matches
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The protein is a recombinant product of a gene fusion construct.

The sequence of the synthetic hirudin HV-1 genes was designed
assed on the published amino acid sequence (bodd J., et al FEBS
Letters 165 180 (1984).

Letters 165 180 (1984).

From Eck amplified chromosomal DNA from S. equisimilis ATCC 10009
C or ATCC 5642.

The primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, Ished DNA sequence or construct an expression vector in which the hirudin gene is linked to the streptokinase gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is sequence encoding a cleavage site for factor Xa.

C released specifically at the place where clot formation is occurring. See also AAR12887-R12889, AAR12891-R12894 and AAR12522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                    Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis.
                                                                                                                                                                                                                                                                                                                                                                                          66..69
/label= linker
/note= "factor Xa cleavage site"
                                                                                                                      Factor Xa-cleavable hirudin-IEGR-streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70..483
/label= streptokinase
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..65
/label= hirudin HV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 96; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRBI-) BRITISH BIO-TECHNOLOGY LTD
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89GB-0027722.
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                                                (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dawson KM, Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-208151/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ12162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-1990;
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07-DEC-1989;
                                                25-MAR-2003
17-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409109125-A
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                                                                                                                                                                                                                                                              Synthetic
AAR12885;
                                                                                                                                                                                                                                                                                                                    Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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Local Similarity 100. nes 6; Conservative

Matches

Query Match

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Gaps

; 0

100.0%; Score 30; DB 23; Length 440; 100.0%; Pred. No. 82; ive 0; Mismatches 0; Indels (

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1 SVDVEY

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The protein is a recombinant product of a gene fusion construct.

The sequence of the synthetic hirudin HV-1 genes was designed
assed on the published amino acid sequence (bodd J., et al FBBS
Letters 165 180 (1984). The sequence of streptchinase was obtd.

From PCR amplified chromosomal DNA from S. equisimilis ATCC 10009

or ATCC 9642. The primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]).

Esquences were used to construct an expression vector in which the streptchinase gene is linked to the hirudin gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also AAR12889. ARR12891-R12894 and AAR12885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein cleavage by blood clotting enzyme - for prodn. of
fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 30; DB 12; Length 483; Best Local Similarity 100.0%; Pred. No. 91; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                               Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis.
                                                                                                                                                                                                                                                                                                                                                                /label= linker
/note= "factor Xa cleavage site"
                                                                                                                                                                                                     Factor Xa-cleavable streptokinase-IEGR-hirudin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Czapleswski LG;
                                                                                                                                                                                                                                                                                                                          1..414
/label= streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 96; 115pp; English
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BRBI-) BRITISH BIO-TECHNOLOGY LTD
                                                                                                 AAR12522 standard; Protein; 483 AA
                                                                                                                                                                                                                                                                                                                                                                                               419..483
/label= hirudin
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                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-208151/28
                           226 SVDVEY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 AA;
SVDVEY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1990;
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                                                                                                                                                            25-MAR-2003
17-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dawson KM,
                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                 AAR12522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                        AAR1252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pusion protein cleavage by blood clotting enzyme - for prodn. of
fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                      1..85
/label= pre-pro alpha factor secretion sequence
/note= "S. cerevisiae"
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0
                                                                                                                                                                                      Streptokinase fused to yeast alpha factor secretion sequence.
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                                                                                                                                                                                                                  Pusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase.
                                                                                                                                                                                                                                                          streptococcus equisimilis ATCC 9542 or ATCC 100009
                                                                                                                                                                                                                                                                                                                                            86..499
/label= mature streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 86; 115pp; English.
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
                                                                                           AAR12891 standard; Protein; 499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           90WO-GB01911
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89GB-0027722
                                                                                                                                                              (first entry)
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                                                                                                                                                 (updated)
            ||||||
157 SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-208151/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 SVDVEY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ12158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-1990;
07-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prophylaxis.
                                                                                                                                                 25-MAR-2003
                                                                                                                                                              17-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                       409109125-A.
                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                        AAR12891;
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Best Local S
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Peptide
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Matches
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The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clotes. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising a administering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for a bacterial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. Streptokinase can also be used in non-human mammals. Streptokinase activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least to a emino acid substitution that confident a substitution of the streptokinase at least two-fold. The present crace of degradation of the streptokinase at least two-fold. The present crace of degradation of the streptokinase at least two-fold. The present crace of degradation of the streptokinase at least two-fold.
myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis, arterial thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus equisimilis ATCC 9542 or ATCC 100009,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 20;
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Met-core streptokinase-core streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 55-58; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                             N-terminally deleted streptokinase
                                                                                                                                                                                            98WO-US26694.
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Query Match
Best Local Similarity 100....
Best Acadesis
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(first entry)
                                                           Streptococcus equisimilis
                                                                                                                                                                                                                                                                     HARD ) HARVARD COLLEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 736 AA;
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                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX83589
                                                                                                                                                                                              .5-DEC-1998;
                                                                                                                      409931247-A1
                                                                                                                                                                                                                                    15-DEC-1997;
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17-SEP-1991
                                                                                                                                                           24-JUN-1999.
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                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                              Reed GL;
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AAR12894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Imparting injectable fibrinolytic agent - with affinity for intravascular thrombus, by linking agent to fibrin binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The conjugate comprises an FB-FB dimer linked to streptokinase The FB fragment has selective affinity for fibrin, low affinity for fibrinogen, and minimal immunogenicity, imparting thrombustargetting capability.
See also AAR11821 and AAR11828.
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                                                                                                                                                                                                Fibrin-binding protein; fibrinolysis; intravascular thrombi; fibrinogen; streptokinase; fusion protein.
                                                                                                                                                                                                                                                                                                                                                    62..119
/label= FB monomer
120..531
/label= streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant streptokinase rSK60-414.
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY24798 standard; Protein; 736 AA.
                                                                                                                                                                                                                                                                                                                    2..61
/label= FB monomer
                                             AAR11829 standard; Protein; 531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87US-0099242
89US-0437769
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                                                                                                                           08-JUL-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CREA-) CREATIVE BIOMOLEC.
                                                                                                                                                                 FB-FB-SK fusion conjugate
                                                                                                                                                                                                                                                             Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-140198/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ11651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5011686-A
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                                                                                      AAR11829;
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Key Protein

Protein

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composition comprision uservices an interestriction in a pharacceutical composition comprising an isolated modified streptokinase, the composition comprising an isolated modified streptokinase, the composition comprising an isolated modified streptokinase, the modification being removal of anion acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; che expression vector comprising (1); and (4) a host cell transformed with expression vector comprising (1); and (4) a host cell transformed with a bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thrombosic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase a streptokinase has at least one amino acid substitution that modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proteolytic cleavage. The present can example of the streptokinase at least two-fold. The present sequence represents a streptokinase and maltose binding protein fusion correction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated bacterial protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasminogen-binding fragment; streptokinase; degradation;
thrombolytic agent; blood clot; bolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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11arity 100.0%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasminogen-binding domain from streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW21723 standard; protein; 800 AA.
                                                                                                                                                                                                                                                                                                                                                                     N-terminally deleted streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 48-51; 73pp; English
                                                                                                                             98WO-US26694
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                                                                                                                                                                                                             (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                      WPI; 1999-395183/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 SVDVEY 543
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              795 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX80497
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                                                                                                                                                                       15-DEC-1997;
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                                                                                                                               15-DEC-1998;
                                          WO9931247-A1
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                                                                                    24-JUN-1999
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  Synthetic.
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                                                                                                                                                                                                                                                            Reed GL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus, streptokinase, fibrin-dependent plasminogen activator, nSK, rSK, bacterial, blood clot, thrombotic condition, myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis, arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence was deduced from DNA obtd. from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C) ATCC 10009 or ATCC 9642. The gene was tuncated by 15 codons at the 3' terminal and one copy engineered to add a Met codon prior to codon 16 of the CDS. The two truncated genes were used to construct an expression vector in which they were linked via a sequence encoding a cleavage site for thrombin which, when cleaved, releases the individual proteins which have antithrombotic activity. The thrombin is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also AAR12887-R12889, AAR12891-R12893, AAR12885 and AAR12522. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein cleavage by blood clotting enzyme - for prodn. of
fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptokinase and maltose binding protein fusion protein.
                                                                                                                 370..379
/label= thrombin cleavage site
                                              2.369
/label= core streptokinase
/note= "AAs 16-383"
                                                                                                                                                     380.747
|Jabel= core streptokinase
|note= "AAs 16-383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 93, 115pp; English
                             location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
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89GB-0027722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVDVEY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-208151/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               747 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ12161
                                                                                                                      Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-1999
                                                                                                                                                                                                                                                                                                                                      07-DEC-1990;
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                                                                                                                                                                                                                                                   WO9109125-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dawson KM,
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Sequence

143

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AAY24797;

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Gaps

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us-09-919-703-1.open.rag

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and prophylaxis.
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; major outer membrane protein A;
of streptokinase. This fragment was used in the design of a modified streptokinase has an in vitro degradation rate at le 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, opt. as a bolus rather than by continuous infusion.
                                                                                                                                                Length 813;
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus equisimilis ATCC 9542 or ATCC 100009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436..445
/label= linking peptide
/note= "cleavage site for thrombin"
                                                                                                                                                  100.0%; Score 30; DB 18; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ទី
                                                                                                                                                                                                                                                                                                                                                                                                                  OmpAL streptokinase-streptokinase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..21
/label= OmpAL signal s
/note= "from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22..435
/label= streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Czapleswski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 90, 115pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                             AAR12893 standard; Protein; 859 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90WO-GB01911.
89GB-0027722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90WO-GB01911
                                                                                                                                     Ouery Match
Query Match
Best Local Similarity 100.vv
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dawson KM, Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-208151/28
                                                                                                                                                                                                                                      SVDVEY 161
                                                                                                                         813 AA;
                                                                                                                                                                                                            1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ12160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-1990;
07-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombin; as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
17-SEP-1991
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                                                                                                                                                                                                                                                                                                                                         AAR12893;
                                                                                                                          Sequence
                                                                                                                                                                                                                                        156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                  RESULT 59
AAR12893
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                                                                                                                                                                                                                                                                                                                            888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                  Modified forms of streptokinase resistant to enzymatic cleavage -
useful as thrombolytic agents in treating thrombosis and in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified forms of streptokinase resistant to enzymatic cleavage - useful as thrombolytic agents in treating thrombosis and in medical equipment
                                                                                                                                                                                                                                                  This sequence represents the plasminogen-binding fragment of streptokinase which lacks the N-terminal 14 amino acids. This modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, opt. as a bolus
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wild type plasminogen-binding fragement of Streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 30; DB 18;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 12-13; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW21728 standard; protein; 813 AA.
                                                                                                                                                                                                                          Claim 2; Page 35-37; 65pp; English
                                                                                                                                                                                                                                                                                                                                                         rather than by continuous infusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US09640
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                            96WO-US09640
                                                      95US-0488940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                  (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-065469/06
                                                                                                                                          WPI; 1997-065469/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 SVDVEY 148
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      800 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1996;
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                            07-JUN-1996;
                                                        09-JJN-1995;
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                                                                                                                                                                                                   equipment
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                Reed GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
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This sequence represents the wild type plasminogen-binding fragment

Length 1181;

DB 18;

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                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified forms of streptokinase resistant to enzymatic cleavage - useful as thrombolytic agents in treating thrombosis and in medical
denes are linked via a sequence encoding a cleavage site for thrombin which, when cleaved, releases the individual proteins which have anti-thrombotic activity. The thrombin is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also AAR12887-R12889, AAR12891-R12894, AAR12885 and AAR12522. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptokinase/maltose binding protein fusion protein, rSKdeltal4
                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasminogen-binding fragment; streptokinase; degradation; MBP;
thrombolytic agent; blood clot; bolus; maltose-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Has N-terminal 14 amino acids deleted"
                                                                                                                                                            100.0%; Score 30; DB 12; Length 859; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.381
/label= Maltose binding protein
/label= acts as blocking group"
382.1181
/label= Modified_Streptokinase
                                                                                                                                                                                                                                                                                                                                          AAW21727 standard; protein; 1181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 12; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus equisimilis
                                                                                                                                                Query Match
Best Local Similarity 1000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-065469/06.
                                                                                                                                                                                                                                                           178 ŚVDVEY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1181 AA
                                                                                                                                   859 AA;
                                                                                                                                                                                                                             1 SVDVEY 6
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                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reed GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                            RESULT 60
AAW21727
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                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified forms of streptokinase resistant to enzymatic cleavage - useful as thrombolytic agents in treating thrombosis and in medical equipment
                                                                                                                                                                                                                                     Plasminogen-binding fragment; streptokinase; degradation; MBP; thrombolytic agent; blood clot; bolus; maltose-binding protein.
                       ö
                        Indels
        red. No. 2.5e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                        ...381
|abel= Maltose_binding_protein
|note= "acts as_blocking_group"
                                                                                                                                                                                                                                                                                                                                                                            label= Modified_streptokinase
100.0%; Score 30;
100.0%; Pred. No. 2
ive 0; Mismatche
                                                                                                                                     AAW21724 standard; protein; 1194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 41-44; 65pp; English
                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                              Modified streptokinase, rSK5mut
                                                                                                                                                                                                                                                                                                                                                                                                    label= R10A
                                                                                                                                                                                                                                                                                                                                                                                                                           label= R36A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= R51A
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                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                          Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                               ..1194
                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     label=
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                                                                         529
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 393
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                                                  1 SVDVEY
                                                                          524 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                              61
                         Matches
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Modified forms of streptokinase resistant to enzymatic cleavage -
useful as thrombolytic agents in treating thrombosis and in medical
equipment
                                                                                                     Plasminogen-binding fragment; streptokinase; degradation; MBP;
thrombolytic agent; blood clot; bolus; maltose-binding protein.
          AAW21725 standard; protein; 1194 AA.
                                                                              Modified streptokinase, rSK6mut.
                                                        (first entry)
                                                                                                                                       Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-065469/06.
                                                                                                                                                                                                                                                                                         Misc-difference 426
                                                                                                                                                                                                                                                                                                                Misc-difference 432
                                                                                                                                                                                                                                                                                                                                       Misc-difference 440
                                                                                                                                                                                                                                             Misc-difference 39.
                                                                                                                                                                                                                                                                   Misc-difference 41'
                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                        01-OCT-1997
                                                                                                                                                    Synthetic.
                                 AAW21725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed GL;
                                                                                                                                                                                     Protein
                                                                                                                                                                                                                        Protein
AAW21725
ID AAW2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a fusion protein between maltose-binding protein and the plasminogen-binding fragment of streptokinase. This fusion protein was used in the design of modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood colots in vivo in a mammal, preferably at a dose of 20000 U/kg, optionally as a bolus rather than by continuous infusion.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified forms of streptokinase resistant to enzymatic cleavage -useful as thrombolytic agents in treating thrombosis and in medical equipment
                                 ö
                                                                                                                                                                                                                                Plasminogen-binding fragment; streptokinase; degradation; MBP; thrombolytic agent; blood clot; bolus; maltose-binding protein.
        Query Match 100.0%; Score 30; DB 18; Length 1194; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 100.0%; Score 30; DB 18; Length 1194; Local Similarity 100.0%; Pred. No. 2.5e+02; les 6; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                          Streptokinase/maltose binding protein fusion protein, rSK
                                                                                                                                                                                                                                                                                                 1.381
/label= Maltose binding protein
/note= "acts as blocking group"
382.1194
/label= Streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 11-12; 65pp; English
                                                                                                                                     AAW21726 standard; protein; 1194 AA.
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0488940.
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                                                                                                                                                                                                                                                                  Streptococcus equisimilis.
                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-065469/06.
                                                                            537 SVDVEY 542
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                                                        1 SVDVEY
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                                                                                                                                                             AAW21726;
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                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                RESULT 62
                                                                                                                            AAW21726
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/label= K185A /note= "Given in the specification as K386A"

95US-0488940 96WO-US09640

label= R59A

/label= Maltose binding protein /note= "acts as blocking group" 382. 1194 /label= Modified\_streptokinase

label= R36A label= R45A label= R51A

/label= R10A

Location/Qualifiers

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                                                   This sequence represents a fusion protein between maltose-binding protein and a modified form of the plasminogen-binding fragment of streptokinase containing 6 point mutations. This modified streptokinase has an in vitro degradation rate at least 2 times slower than that of native streptokinase. Compounds containing modified streptokinases are specifically used as thrombolytic agents for dissolving blood clots in vivo in a mammal, preferably at a dose of 20000 U/kg, optionally as a bolus rather than by continuous infusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 30; DB 18; Length 1194; 100.0%; Pred. No. 2.5e+02; Live 0; Mismatches 0; Indels 0.
Claim 16; Page 44-48; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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SVDVEY 542

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1 SVDVEY 6

Matches

Search completed: January 20, 2004, 14:58:47 Job time : 42 secs

AAY01550
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AAR10196
AAR10196
AAR12892
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AAR10195
AAR10195

AAY84007 AAR10199 AAY25020 AAY84005 ABB80012 ABB801094 AAR10194 AAR23120 AAY24734 AAY24734 AAY24734 AAY24734 AAY24734 AAY3456

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; Search time 42 Seconds (without alignments) 22.675 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1985.DAT:*
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         GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Streptokinase deri				Streptokinase deri		Streptokinase frag		
SUMMARIES	QI	AAY25009	ABB80001	ABB80005	AAY25013	AAY25014	ABB80006	ABG76052	AAY25015	ABB80007
		20	23	23	20	50	23	24	20	23
	Query Match Length DB	9	Q	16	18	20	20	20	21	21
% Query Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	30	30	30	30	30	30	30	30	30
	Result No.	٦	7	m	4	Ω	9	7	œ	σ

Recombinant strept
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Recombinant strept
Truncated Met strept
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Streptokinase (1-3
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Streptococcus sp.
Streptokinase (3k)
Streptococcus sp.
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Streptokinase (4ki)
Streptokinase (4ki) Propionibacterium Novel human diagno Leptospira membran Galid herpesvirus

AAW86143 AAW86144 AAW86144 AAB01296 AAB01296 AAB01296 AAY50870 AAY50870 AAY50870 AAY12889 AAR12889 AAR12889 AAR12891 AAR12891 AAR12891 AAR12891 AAR12891 AAR12893 AAR1728 AAR12893 AAR1728 AAR1728

**ALIGNMENTS** 

RESULT 1

Complexionase; cell death; amelioration; treatment; disease; aging; AIDS; cellular differentiation; physical insult; treuma; anoxia; hyperthermia; whypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease, Alzheimer's disease; Huntington's disease; Cerebellar deceneration; cardiovascular disease; Maintington's disease; cerebellar deceneration; cardiovascular disease; milat amyotrophic lateral sclerosis; atheritis; renal; retinal; we familial amyotrophic lateral sclerosis; atheritis; renal; retinal; reperfusion injury; immune disease; rheumatoid arthritis; renal; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; spenicious anaemia; dermatomyopathy; hypertensive; myasthenia gravis; pernicious anaemia; dermatomyositis; enythema nodosum; wasthenia gravis; spenicious anaemia; dermatomyositis; enythema nodosum; neuroma; melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; mon-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; mon-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; pancreatitis, Crohn's disease; ulcerative colltis; motor neuron disease; who chemotherapy; clozapine; AZT; anthracycline. Streptokinase derived peptide 1 for amelioration of cell death. AAY25009 standard; peptide; 6 AA. (first entry 23-AUG-1999 Synthetic. AAY25009; 

US5917013-A.

29-JUN-1999

96US-0759599. 05-DEC-1996;

95US-0008233 96US-0759599 06-DEC-1995; 05-DEC-1996;

(RABK/) RABKIN S W.

Krystal G, Rabkin SW;

WPI; 1999-394231/33

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 2; Column 12; 15pp; English.

AAY25009-Y25019 are novel peptides derived from streptokinase that

ameliorate cell death. The products of the invention and their encoding

uclaid acids may be useful for treating diseases and conditions related

to aging, cellular differentiation, physical insult (e.g. physical

trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,

and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin

cond any other organ), viral disorders (e.g. hepatitis, retroviral

infections, viral encephalitis, and AID5/HIV), neurodegenerative

ci disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's

ci serceis (FALS)), cardiovascular disease (e.g. atherosclerosis,

consciential infarction, heart failure, cardiomyopathy, myocardial

creperfusion injury, and hypertensive heart disease), immune disease (e.g.

rheumatoid arthritis, systemic lugus erythematosus, insulin-dependent,

diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema

condosum, Sigoran's systomic lugus erythematosus, insulin-dependent,

diabetes mellitus, lupus, pernicious anaemia, dermatomyositis,

wegener's granulomatosis, glomerulonephritis, myasthenia gravis,

condosum, Sigoran's systomic lugus erythematosus, and avoits

condosum, sigorathritides), a neoplastic disorder (e.g. leukemia,

condosum, sigorathritides), a neoplastic disorder (e.g. leukemia,

concass, myelomas, carcinomas, melanomas, cancers of the

con-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint

disorders and inflammatory induced cell damage to the eye, brain and

New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

Krystal G, Rabkin SW;

WPI; 2002-266542/31.

Claim 3; Column 5; 18pp; English

ö The probabilities; antiparkinsonan; anticonvulsant; cytostatic;

A netinfilammatory; antiarkinsonan; anticonvulsant; cytostatic;

A netinfilammatory; antiarkhritic; antirheumatic; cardiant;

W antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;

W dermatological; antidiabetic; antiamemic; virucide; ophthalmological;

W antiulcer; antibacterial; antiparastitic; heurodegenerative disease;

W arkinson's disease; Alzheimer's disease; Huntington's disease;

W erebellar degeneration; neoplastic disorder; cancer;

W ardiovascular disease; heart failure; atherosclerosis;

W ardiovascular disease; heart failure; atherosclerosis;

M mycardial reperfusion injury; immune disease; autoimmune disease;

W systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;

W myelodegenerative diseases; viral diseases; macular degeneration;

W carlant; Crohn's disease; viral diseases; macular degeneration;

W carlant; Crohn's diseases; ulcerative colitis; pancreatitis; other organs), ischemia or reperfusion injury (e.g. myocardial ischemia and reperfusion injury, renal ischemia, spinal cord ischemia and/or reperfusion injury, retinal ischemia or infarction, and stroke), toxic insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other organs from chemicals, radiation, and other noxious substances), macular degeneration, cataract formation, pancreatitis, Crohn's disease, ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord Guillan Bare Syndrome and demyellnating disease), bypass surgery, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT, Gaps .. 100.0%; Score 30; DB 20; Length 6; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels Streptokinase; cell death; apoptosis; necrosis; nootropic; (MOLE-) MOLECULAR THERAPEUTICS INC. ABB80001 standard; peptide; 6 AA. Streptokinase derived peptide#1. 99US-0294457. 95US-008233P. 96US-0759599. (first entry) Conservative prion disease; aging and anthracyclines. Best Local Similarity Matches 6; Conserv 1 SVDVEY 6 6 AA; 1 SVDVEY US6348567-B1. 26-JUL-2002 19-APR-1999; 06-DEC-1995; 05-DEC-1996; 19-FEB-2002. Synthetic. Sequence ABB80001; Query Match RESULT 2 ABB80001 ઠે

The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, neuroprocective, antiparkinsonian, anticonvulsant, cytostatic, antinatherosclerotic, vasotropic, immunosuppressive, anti-HIV controlled, antiutidabetic, antianaemic, virucide, ophthalmological, antidabetic, antianaemic, virucide, ophthalmological, antidabetic, antianaemic, virucide, ophthalmological, antidabetic, antianaemic, virucide, ophthalmological, antidabetic, antianaemic, virucide, ophthalmological, antidaces apoptosis and antiparasitic. Peptides of the invention ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions comprising peptides of the invention are useful for treating concurration diseases (e.g. Alzheimer's, Huntington's disease and cerebellar degeneration) neoplastic disorders including cancer, inflammatory disorders (e.g. arthritis, inflammatory joint disorders (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune diseases, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis, systemic lupus erythematosus, diabetes mellitus, pernicious anaemia), myolodegenerative diseases, viral diseases, and degenerative diseases of any organ. Other disorders include macular degeneration, cataracts, crohn's diseases, ulcerative oolitis, cataracts, pancreatitis, infectious diseases, and desire. The current sequence represents a streptokinase accelerated aging. The current sequence represents a streptokinase of derived beptide of the invention with an ability to ameliorate cell Length 6; death in cardiac myocytes. 6 AA; Sequence 

0; Indels 100.0%; Score 30; DB 23; 100.0%; Pred. No. 9.3e+05; Mismatches . 0 Local Similarity 100. Les 6; Conservative 9 1 SVDVEY 6 1 SVDVEY Query Match Matches ð g

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Gaps

; 0

ABB80005 standard; peptide; 16 AA

(first entry) 26-JUL-2002

Streptokinase derived peptide#5.

Streptokinase; cell death; apoptosis; necrosis; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; cytostatic; antilnflammatory; antilartheritic; cardiant; antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV; dermatological; antidiabetic; antianaemic; virucide; ophthalmological; antibacteritial; antiparasitic; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; Huntington's disease; cerebellar degeneration; neoplastic disorder; cancer; inflammatory disorder; arthritis; inflammatory joint disorders; carddovascular disease, heart failure; atherosolerosus; myocardial reperfusion injury; immune disease; autoimmune disease; acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis; systemic lupus erythematosus; diabetes mellitus; pernicious anaemia; myelodegenerative disease; viral diseases; macular degeneration; cataract; Crohn's disease; ulcerative colitis; pancreatitis; prion disease; aging 

Synthetic

19-FEB-2002

99US-0294457 .9-APR-1999;

95US-008233P. 96US-0759599. 06-DEC-1995; 05-DEC-1996;

(MOLE-) MOLECULAR THERAPEUTICS INC

Krystal G, Rabkin SW,

WPI; 2002-266542/31.

New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

Claim 7; Column 5; 18pp; English

peptides of the invention may be described as, mostropic, concurrent convoluent, cytostatic, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, antidabetic, antianaemic, virucide, ophthalmological, dermatological, antidabetic, antianaemic, virucide, ophthalmological, antidacerial and antiparasitic. Peptides of the invention ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions comprising peptides of the invention are useful for treating comprising peptides of the invention neoplastic disorders including cancer, inflammatory disorders (e.g. heart failure, atherosclerosis cancer, inflammatory disorders (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune conservation injury), immune diseases, and degenerative diseases (e.g. my organ. Other disorders include macular degeneration, cataracts, conservative diseases, ulcerative colitis, cataracts pancerative diseases, ulcerative colitis, cataracts pancerative diseases. The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, diseases including bacteria, parasite, prion-based diseases, and accelerated aging. The current sequence represents a streptokinase derived peptide of the invention with an ability to ameliorate cell death in cardiac myocytes.

16 AA; Sequence

Gaps . 100.0%; Score 30; DB 23; Length 16; 100.0%; Pred. No. 1.9; ive 0; Mismatches 0; Indel9 6; Conservative Query Match Best Local Similarity Matches 6; Conserv

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RESULT 4 AAY25013

AAY25013 standard; peptide; 18 AA.

AAY25013;

(first entry) 23-AUG-1999 Streptokinase derived peptide 5 for amelioration of cell death.

Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; cellular differentiation; physical insult; trauma; anoxia; hyperthermia; W hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; Huntington's disease; cerebellar degeneration; cardiovascular disease; W familial amyorrophic lateral sclerosis; atherosale; heart failure; infarction; heart disease; retunapopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lupus erythematosus; insulin-dependent; diabetes mellitus; w pernicious anneania, dermatomyositis; enythema nodosum; myasthenia gravis; sjogren's syndrome; temporal arthritis; autoimmune polyarthritides; w Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome; meoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;

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XX XX AV25009-Y25019 are novel peptides derived from streptokinase that cameliorate cell death. The products of the invention and their encoding conciled may be useful for treating diseases and conditions related to aging, cellular differentiation, physical insult (e.g. physical conciled may be useful for treating diseases and conditions related to aging, cellular differentiation, physical insult (e.g. physical concentration, and prothermia, chemically induced damage, and any other organ), viral encephalitis, and AIDS/HIV), neurodegenerative disease, cerebellar degenerations, and familial amyotrophic lateral collections, viral encephalitis, and AIDS/HIV), neurodegenerative disease, cerebellar degenerations, and familial amyotrophic lateral collections (FALS), cardiovascular disease (e.g. atherosclerosis, collections, and hypertenaive heart disease), immune disease (e.g. myocardial infarction, heart failure, cardiomyopathy, myocardial collections, nad hypertenaive heart disease), immune disease (e.g. creperfusion injury, and hypertenaive heart disease), immune disease (e.g. myotardial disease), and autoimmune polyarthritides), a neoplastic disorder (e.g. lukemia, carcinomas, myelomas, carcinomas, melanoma, cancers of the breast, brain, colon, cervix, and prostate, hodgkin's disease and con-Hodgkin's lymphomal, inflammatory discorders (e.g. inflammatory joint disorders and inflammatory discorders (e.g. inflammatory discorders (e.g. inflammatory discorders), macular colon, cervix, and prostate, hodgkin's lymphomal, inflammatory discorders (e.g. inflammatory discorders), macular colon, cervix, and prostate, hodgkin's lymphomal, inflammatory discorders (e.g. inflammatory induced cell damage to the eye, brain and colon, cervix, and prostate, appinal cord ischemia and cord incoming the e.g. incoming and concentration injury, retinal ischemia or infarction, and stroke), macular concents in acceleration, and other noxious substenaces), macular degeneration cataract formation, panceratitis, collisses (e.g. e.g. e.g. e.g.
melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; pancreatitis, Crohn's disease; ulcerative colitis; motor neuron disease; Guillan Bare Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Column 12; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                 95US-0008233.
                                                                                                                                                                                                                                                                                                                    96US-0759599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krystal G, Rabkin SW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-394231/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (RABK/) RABKIN S W.
                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1995;
                                                                                                                                                                                                                                                                                                                       05-DEC-1996;
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                                                                                                                                                                                                                           US5917013-A.
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                                                                                                                                                                           Synthetic.
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18 AA; Sequence

neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome and demyelinating disease), bypass surgery, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT,

100.0%; Score 30; DB 20; Length 18; 100.0%; Pred. No. 2.2; Live 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches 6; Conserv

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Gaps

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XX Streptokinase, cell death, amelioration; treatment; disease, aging; AIDS, Cellular differentiation; physical insult; trauma; anoxia; hyperthermia; XX byfothermia; brain; spinal cord; kidney; heart; lung; llver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; nurial disorder; parkinson's disease, Alzheimer's disease; Mintangton's disease; atherial; cardiovascular disease; Mintangton's disease; atherosclerosis; heart failure; Mintangton's disease; ardiowyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; XX reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; XX perfusion injury; immune disease; rheumatoid arthritis; renal; retinal; XX perfusion injury; immune disease; rheumatoid arthritis; renal; retinal; No pernicious anaemia; dermatomyositis; enthema nodosum; myasthenia gravis; No spens asyndrome; temporal arthritis; autoimmune polyarthritides; hegener; sgranulomatosis; glomerulomephritis; auti-phospholipid syndrome; moplastic disorder; leukemia; sarcoma; myeloma; cancer; breast; colon; cervix; prostate; Hoddkin's disease; hoddkin's lymphoma; inflammatory disorder; stroke; ischemia; mon-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; whilm an are Syndrome; demyelinating disease; bypass surgery; chemotherapy; clozapine; AZT; anthracycline. Streptokinase derived peptide 6 for amelioration of cell death. AAY25014 standard; peptide; 20 AA. (first entry) 23-AUG-1999 AAY25014; AAY25014 

Synthetic.

JS5917013-A.

29-JUN-1999

96US-0759599. 05-DEC-1996; 95US-0008233. 96US-0759599. 06-DEC-1995; 05-DEC-1996;

(RABK/) RABKIN S W.

Rabkin SW; Krystal G,

WPI; 1999-394231/33.

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 7; Column 12; 15pp; English.

AAY25009-Y25019 are novel peptides derived from streptokinase that

ameliorate cell death. The products of the invention and their encoding

nucleic acids may be useful for treating diseases and conditions related
to aging, cellular differentiation, physical insult (e.g. physical

trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,
and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin
and any other organ), viral disorders (e.g. hepatitis, retroviral
infections, viral encephalitis, and AIDS/HV), neurodegenerative
disorders (e.g. Parkinson's disease, Altheimer's disease, Huntington's
clerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,
myocardial infarction, heart failure, cardiomyopathy, myocardial
cheumatoid arthritis, systemic lupus erythematosus, immune disease (e.g.
cheumatoid arthritis, systemic lupus erythematosus, insulin-dependent,
diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema
nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,
medoener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,
and autcimmune polyarthritides), a neoplastic disorder (e.g. leukemia,
sarcomas, myelomas, neuromas, melanoma, cancers of the

Claim 8; Column 5; 18pp; English.

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breast, brain, colon, cervix, and prostate, Hodgkin's disease and non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint disorders and inflammatory induced cell damage to the eye, brain and other organs), ischemia or reperfusion injury (e.g. myocardial ischemia and reperfusion injury, renal ischemia, spinal cord ischemia and/or reperfusion injury, retinal ischemia or infarction, and stroke), toxic reperfusion injury, retinal ischemia or infarction, and stroke), toxic organs from chemicals, radiation, and other noxicus substances), macular degeneration, cataract formation, and other noxious substances), macular degeneration, cataract formation, pancreatitis, Crohn's disease, ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome and demyelinating disease), bypass surgery, chemotherapy, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       and anthracyclines.
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20 AA; Seguence

.; 0 Gaps ; 0 100.0%; Score 30; DB 20; Length 20; 100.0%; Pred. No. 2.4; ive 0; Mismatches 0; Indel8 Local Similarity 100. Query Match Matches Best

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ABB80006 standard; peptide; 20 AA.

ABB80006;

Streptokinase derived peptide#6.

26-JUL-2002 (first entry)

Streptokinase; cell death; apoptosis; necrosis; nootropic;

neuroprotective; antiparkinsonian; anticonvulsant; cytostatic; antinflammatory; antiarthritic; antirheumatic; cardiant; antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV; dermatological; antidabetic; antianaemic; virucide; ophthalmological; antiulcer; antibacterial; antiparessitic; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; Huntington's disease; cerebellar degeneration; neoplastic disorder; cancer; inflammatory disorder; arthritis; inflammatory joint disorders; cardiovascular disease; heart failure; atherosclerosis; myocardial reperfusion injury; immune disease; autoimmune disease; acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis; mystemic lupus erythematosus; diabetes mellitus; pernicious anaemia; myelodegenerative diseases; viral diseases; macular degeneration; cataract; Crohn's disease; ulcerative colitis; pancreatitis; 

Synthetic.

prion disease; aging

US6348567-B1.

.9-FEB-2002.

99US-0294457. 95US-008233P. 96US-0759599. 19-APR-1999; 06-DEC-1995;

05-DEC-1996;

MOLE-) MOLECULAR THERAPEUTICS INC.

Krystal G, Rabkin SW;

WPI; 2002-266542/31.

New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, autiarthritic, anticonvulsant, cytostatic, antinflammatory intidiabetic, immunosuppressive, anti-HIV, contribacterial and antiparasitic. Peptides of the invention anticorder, ophthalmological, antidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antianaemic, virucide, ophthalmological, antidiacer apoptosis and natiparasitic. Peptides of the invention ameliorates apoptosis and natiparasitic. Peptides of the invention accomprising peptides of the invention awarm-blooded animal. Compositions of the invention neoplastic disorders including concerning and myocardial reperfusion injury), immune diseases (e.g. heart failure, atherosclerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune cy gettemic lugues erythematosus, diabetes mellitus, pernicious anaemia), myolodegenerative diseases, viral diseases, and degenerative diseases of any organ. Other disorders include macular degeneration, cataracts, myelodecentated aging. The current sequence represents a streptokinase contents in the invention with an ability to ameliorate cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 30; DB 23; Length 20; 100.0%; Pred. No. 2.4; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       death in cardiac myocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SVDVEY
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ABG76052 standard; peptide; 20 AA. ABG76052

RESULT 7

(first entry) 20-MAY-2003 Streptokinase fragment based, cell death ameliorating, 20mer peptide.

Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS; Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma; atheroscierosis; myocardial inferction; immune disease; carcinoma; rheumatord arthritis; moplastic disorder; inflammatory disorder; arthritis; inflammatory induced cell damage; motor neuron disease; arthritis; inflammatory induced cell damage; motor neuron disease; physical insult; severe shock; ischaemia; reperfusion injury; hepatitis; cell dath associated procedure; spinal cord reperfusion injury; toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease; duillain-Bare syndrome; bypass surgery; myocardial ischaemia; chenotherapy; viral disease; viral encephalitis; infectious disease; bacterial disease; prion-based disease; macular degeneration; cataract formation; pancreatitis; Crohn's disease; ulcerative colitis; accelerated aging; oxidative stress. 

Synthetic.

JS2002165129-A1.

07-NOV-2002.

31-JUL-2001;

95US-008233P. 99US-0294457. 06-DEC-1995; 19-APR-1999;

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The invention relates to a pharmaceutical composition, which comprises a peptide capable of ameliorating cell death, its derivative or analogue, comprising a sequence Val-Asp-Val, where the peptide is in a suitable paramaceutical carrier or diluent. The pharmaceutical composition composition the peptide) is useful for treating or preventing cell death associated with a neurodegenerative disorder e.g. Parkinson's disease and Alzheimer's disease, cardiovascular disease e.g. Parkinson's disease and Alzheimer's neoplastic disorders e.g. leukseemia and carrinoma; inflammatory disorder e.g. arthritis and inflammatory induced cell damage; disease caused by physical insult e.g. trauma and spinal cord cischaemia or reperfusion injury e.g. myocardial ischaemia and spinal cord reperfusion injury; toxic insult e.g. liver toxicity and pulmonary toxicity; spinal cord disease e.g. motor neuron disease and Guillain-Bare syndrome; procedures associated with cell death e.g. bypass surgery and chemotherapy; viral disease e.g. hepatitis and viral encephalitis; infactious diseases e.g. hepatitis and viral encephalitis; infactious diseases e.g. hepatitis and viral encephalitis; infactious diseases e.g. hepatitis and viral encephalitis; unacultar degeneration; cataract formation; pancreatitis; Crohn's disease; ulcerative colitis; accelerated aging and oxidative stress in a warm-biooded animal. The present sequence represents the amino acid sequence of a generating cell death which is based on a contractive interesting cell death which is based on a
                                                                                                                                                                                                                                     Pharmaceutical composition for treating e.g. neurodegenerative disorder, cardiovascular disease, neoplastic disorder, viral disease and immune diseases, comprises a peptide capable of ameliorating cell
                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 3; 19pp; English.
96US-0759599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     streptokinase fragment.
                                                                                                                                  Krystal G, Rabkin SW
                                                                                                                                                                                      WPI; 2003-246673/25.
                                                 (KRYS/) KRYSTAL G.
(RABK/) RABKIN S W.
05-DEC-1996;
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20 AA; Sequence

Gaps . 0 Score 30; DB 24; Length 20; Pred. No. 2.4; 0; Indels Mismatches . 0 100.0%; 6; Conservative Query Match Best Local Similarity Matches

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SVDVEY 1 SVDVEY

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AAY25015 standard; peptide; 21 AA RESULT 8 AAY25015

AAY25015;

(first entry) 23-AUG-1999 Streptokinase derived peptide 7 for amelioration of cell death.

Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; cellular differentiation; physical insult; trauma; anoxia; hyperthermia; bypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV; viral disorder; hepatitis; retroviral; infection; encephalitis; FALS; neurodegenerative disorder; Parkinson's disease; Alzheimer si disease; familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; infarction; heart disease; carebellar degeneration; cardiovascular disease; familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; infarction; heart disease; cardiomyopathy; hypertensive; myocardial; reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal; systemic lupus exythematosus; insulin-dependent; diabetes mellitus; pernicious anaemia; dermatomyositis; enythema nodosum; myasthenia gravis; Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides; Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome; 

neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma; melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia; spinal cord; toxic insult; pulmonary; macular degeneration; cataract; panoreatitis, Crohn's disease; ulcerative colitis; motor neuron disease; Guillan Bare Syndrome; demyelinating disease; bypass surgery; clozapine; AZT; anthracycline.

Synthetic.

USS917013-A

29-JUN-1999

96US-0759599. 05-DEC-1996; 95US-0008233. 96US-0759599. 06-DEC-1995; 05-DEC-1996;

(RABK/) RABKIN S W.

Rabkin SW; Krystal G,

Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation

Claim 8; Column 12; 15pp; English

ANY25009-Y25019 are novel peptides derived from streptokinase that

ameliorate cell death. The products of the invention and their encoding

cnucleic acidsmay be useful for treating diseases and conditions related

to aging, cellular differentiation, physical insult (e.g. physical

trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,

and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin

cn drauma to the brain, spinal cord, kidney, heart, lungs, liver,

and trauma to the brain, apinal cord, kidney, heart, lungs, liver,

and any other organ), viral disorders (e.g. hepatitis, retroviral

cn disorders (e.g. Parkinson's disease, Alzheimer's disease, liver, skin

cn disease, cerebellar degenerations, and familial amyotrophic lateral

colerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,

disease, cerebellar degenerations, and familial amyotrophic lateral

sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,

disease arthitacs, bytemic lupus erythematosus, insulin-dependent,

disease arthitus, lupus, pernacious anaemia, dermatomyositis, enythema

nodosum, Sjogren's syndrome, temporal arthitis, anti-phospholipid syndrome,

descremes, myelomas, carcinomes, pernacional arthitis, anti-phospholipid syndrome,

sarcomas, myelomas, carcinomas, and prostate, Hodgkin's disease and

condosum, sichemia or reperfusion injury (e.g. myocardial ischemia

and terperfusion injury, retinal ischemia or infarotion, and stroke), toxic

disorders and inflammatory induced cell damage to the eye, brain and

cother organs), ischemia or reperfusion injury (e.g. myocardial ischemia

and reperfusion injury, retinal ischemia or infarotion, and stroke), toxic

insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other

corgans from chemicals, radiation, and other noxious substances),

mental descention, cataract formation, pancreatitis, crown, beancher and

degeneration, cataract formation, chemotherany

and demvelination disease, home and pennylanove.

and demvelination diseas and demyelinating disease), bypass surgery, chemotherapy, chemically-induced reperfusion, and therapeutics such as clozapine, AZT, , chemotherapy and anthracyclines.

21 AA; Sequence

Gaps .. 0 100.0%; Score 30; DB 20; Length 21; 100.0%; Pred. No. 2.6; ive 0; Mismatches 0; Indels 6; Conservative Best Local Similarity Matches 6; Conserv Query Match

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1 SVDVEY 6

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1 SVDVEY

accelerated aging. The current sequence represents a streptokinase derived peptide of the invention with an ability to ameliorate cell death in cardiac myocytes.

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Gaps

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0; Indels

0; Mismatches

6; Conservative

1 SVDVEY 6

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SVDVEY

Local Similarity

Best Loca Matches

Query Match

21 AA;

Sequence

888388

100.0%; Score 30; DB 23; Length 21; 100.0%; Pred. No. 2.6;

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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, noctropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antinflammatory, antiarthritic, anticonvulsant, cytostatic, antinflammatory, antiarthritic, anticonvulsant, cardiant, antidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antiparasitic. Peptides of the invention antiulcer, antibacterial and antiparasitic. Peptides of the invention comprising peptides of the invention are useful for treating neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's comprising peptides of the invention are useful for treating cancer, inflammatory disorders in inputitis, inflammatory joint disorders), cardiovascular diseases (e.g. arthritis, inflammatory joint disorders), cardiovascular diseases (e.g. arthritis, inflammatory joint disease, acquired immunodeficiency syndrome (Albs), rheumatory disorders include macular degenerative diseases of and myocardaral repertures include macular degenerative diseases of myologenerative diseases, ulcerative collitis, cataracts, panoreatitis, infectious diseases including bacteria, parasite, prion-based diseases, and
                                                                                                                                                                                                                       Streptokinase, cell death, apoptosis, necrosis, nootropic, neurogrotective; antiparkinsonian; anticonvulsant; cytostatic; neurogrotective; antiparkinsonian; anticonvulsant; cytostatic; antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV; dermatological; antidabetic; immunosuppressive; anti-HIV; antiulcer; antibacterial; antiparasitic; neurodegenerative disease; wartiulcer; antibacterial; antiparasitic; neurodegenerative disease; werebellar degeneration; neoplastic disorder; cancer; inflammatory disorder; arthritis; inflammatory joint disorder; wardiovascular disease; heart failure; atherosclerosis; myocardial reperfusion injury; immune disease; autoimmune disease; acquired immunodeficiency syndrome; AIDS; theumatorid arthritis; acquired immunodeficiency syndrome; AIDS; theumatorid arthritis; was systemic lupus erythematosus; diabetes mellitus; pernicious anaemia; myelodegenerative diseases; viral diseases; macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cataract; Crohn's disease; ulcerative colitis; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR THERAPEUTICS INC.
                                            ABB80007 standard; peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Column 5; 18pp; English
                                                                                                                                                                                   Streptokinase derived peptide#7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0294457.
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                                                                                                                                      (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krystal G, Rabkin SW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prion disease; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-266542/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS6348567-B1
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05-DEC-1996;
                                                                                                                                      26-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                         ABB80007;
RESULT 9
                          ABB8000.
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Antigenic epitope of streptokinase, spanning amino acids 138-208

18-JUN-1999 (first entry)

AAY01550;

AAY01550 standard; peptide; 71 AA.

AAY01550

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                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an antigenic epitope of streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (PI) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. Pl is used in thrombolytic therapy, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                   Antigenic peptide, streptokinase, streptokinase-specific antibody, thrombolytic activity, thrombolytic therapy, glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides which bind streptokinase-specific antibodies useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 20; Length 71; 100.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevent or treat glomerulonephritis and rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Page 5; 44pp; English.
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                                                                                                                                                                                                                                    98WO-US17114
                                                                                                                                                                                                                                                              97US-0055911,
                                                                                                                                                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                             Parhami-Seren B, Reed GL;
                                                                                                                                                      Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-190113/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 SVDVEY 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 AA;
                                                                                                                              rheumatic fever.
                                                                                                                                                                               WO9908698-A1.
                                                                                                                                                                                                                                     18-AUG-1998;
                                                                                                                                                                                                                                                            18-AUG-1997;
                                                                                                                                                                                                           25-FEB-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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AAY01558
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AAY01558 standard; peptide; 146 AA

AAY01558

24-JUN-1999.

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The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising a diministering to the subject a fibrin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for a bacterial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase streptokinase has at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proteolytic cleavage. This present care of degradation of the streptokinase at least two-fold. The present sequence represents recombinant streptokinase, designated rSK144-293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigenic peptide, streptokinase, streptokinase-specific antibody, thrombolytic activity, thrombolytic therapy, glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide corresponding to amino acids 120-352 of streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 20; Length 150; 100.0%; Pred. No. 24; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    Claim 34; Page 67-68; 73pp; English.
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                                                                                                                                                                                                                                                                                                           N-terminally deleted streptokinase
                                                                                                        97US-0069497
                                                               98WO-US26694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                 (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                         1999-395183/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 AA;
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                                                                                                                                                                                                                                                              N-PSDB; AAX80494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rheumatic fever
                                                               15-DEC-1998;
                                                                                                        15-DEC-1997;
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                                                                                                                                                                                              Reed GL;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a peptide corresponding to amino acids 148-293 of streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. P1 is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus; streptokinase; fibrin-dependent plasminogen activator; nSK; rSK; bacterial; blood clot; thrombotic condition; myocardial infarction; venous thrombosis; pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                   Antigenic peptide, streptokinase, streptokinase-specific antibody, thrombolytic activity, thrombolytic therapy, glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                          Peptide corresponding to amino acids 148-293 of streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides which bind streptokinase-specific antibodies useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 30; DB 20; Length 146; 100.0%; Pred. No. 23; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 13; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                          98WO-US17114
                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0055911
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Best Local Similarity 100.00
Best Local Similarity 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parhami-Seren B, Reed GL;
                                                                               (first entry
                                                                                                                                                                                                                                                           Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-190113/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVDVEY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SVDVEY 6
                                                                                                                                                                                                                   rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-1998;
                                                                                                                                                                                                                                                                                                       WO9908698-A1
                                                                                 18-JUN-1999
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Gaps

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98WO-US17114.

18-AUG-1998; 25-FEB-1999

WO9931247-A1

Synthetic

AAY24796;

10

à d RESULT 12

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Streptokinase (1-372, 45-68 deficient).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ono K, Sakata Y,
                                                                                                                                                                                                                                      AAR10196 standard; Protein; 348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY24795 standard; Protein; 356 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 59; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90EP-0113099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89JP-0179432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHARM FACTOR
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogino K,
                                                                                                                                                       183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-016179/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
6; Conserva
                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVDVEY 138
                                297 AA;
                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 AA
                                                                                                                            1 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SAKA ) OTSUKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-1989;
27-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-1990;
                                                                                                                                                                                                                                                                                                  28-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                          EP407942-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Majima E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY24795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 16
AAY24795
ID AAY24
XX
AC AAY24
                                                                                                                                                                                                       RESULT 15
AAR10196
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                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                               The present sequence represents a peptide corresponding to amino acids 120-352 of streptokinase. The specification describes a polypeptide which binds to a streptokinase pecific antibody and prevents the antibody binding to native streptokinase. The specification also describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. Pl is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of streptokinase encoded by a pST-1 HindIII fragment. Recombinant streptokinase can be produced by culturing bacteria transformed with a high efficiency plasmid contg. the streptokinase gene, amplified by using haemolytic Streptococcus as the template and using inducers based on the streptokinase nucleotide sequence. The recombinant streptokinase is used to treat thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           streptokinase; recombinant production; haemolytic Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prepn. of streptokinase - useful for treating thrombus diseases
                                                                                                                                       polypeptides which bind streptokinase-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 30; DB 20; Length 233; 100.0%; Pred. No. 40; ive 0; Mismatches 0; Indels
                                                                                                                                                                                      Disclosure; Page 13; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR91599 standard; Protein; 297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 6-8; 24pp; Chinese.
                                                                                                                                                       useful in thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYSH-) UNIV SHANGHAI MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94CN-0112106
97US-0055911
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                             (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
                                                                           Parhami-Seren B, Reed GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptokinase from pST-1
                                                                                                          WPI; 1999-190113/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-358628/46
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SVDVEY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT29961
18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9527050-A1
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Sequence Query Match

12-OCT-1995

Song H;

Synthetic

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Gaps
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The protein is used as a thrombolytic agent in patients with lung thromboly is myocardial infarction. See also AAQ10230, AAR10195 and AAR10197-R10200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
100.0%; Score 30; DB 16; Length 297; ilarity 100.0%; Pred. No. 52; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 30; DB 12; Length 348; larity 100.0%; Pred. No. 63; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                streptokinase; thrombolytic agent; myocardial infarction.
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The sequence was deduced from DNA obtd. from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C) ATCC 10009 or ATCC 9642.

ATCC 9642.

The gene was truncated by 15 codons at the 3' terminal and engineered to add a Met codon prior to codon 16 of the streptokinase CDS. The construct was used to prepare expression vector p6G606 for prodn. of the streptokinase core molecule.

See also AAR12897-R12893 AAR12891-R12893, AAR12885 and AAR12522.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 30; DB 12; Length 369; Best Local Similarity 100.0%; Pred. No. 67; Matches 6; Conservative 0; Mismatches 0; Indels (
                                            Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase; thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         streptokinase; thrombolytic agent; myocardial infarction.
                                                                                                          Streptococcus equisimilis ATCC 9542 or ATCC 10009
                                                                                                                                                                             2..369
/label= core streptokinase
/note= "AAs 16-383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptokinase (1-372, Phe 118 deleted).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 88; 115pp; English.
                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRBI-) BRITISH BIO-TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10195 standard, Protein, 371 AA
  Truncated Met streptokinase
                                                                                                                                                                                                                                                                                                                                                                90WO-GB01911
                                                                                                                                                                                                                                                                                                                                                                                                                                 89GB-0027722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dawson KM, Hunter MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-208151/28.
N-PSDB; AAQ12159.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                             07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1989;
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                                                                                                                                                                                                                                                                        WO9109125-A.
                                                                                                                                                                                                                                                                                                                 27-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR10195;
                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an isolated bacterial protein that induces fibrin-dependent plasminogen activation in a pharmaceutical composition for dissolving blood clotes. Also described are: (1) a composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a florin-dependent streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; a nucleic acid (1) encoding a modified bacterial streptokinase protein; capterial fibrin-dependent plasminogen activator is useful for the expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator is useful for dissolving blood clots in patients with a thromboois. The modified tromboois, graft thrombosis and arterial thromboois. The modified activation of plasminogen is at least 10-fold, preferably 100-fold greater in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least one amino acid substitution that inactivates a substrate site for proteolytic cleavage. This reduces the rate of degradation of the streptokinase at least two-fold. The present condition of sequence represents recombinant streptokinase, designated rSK59-414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                 Streptococcus, streptokinase, fibrin-dependent plasminogen activator, nSK; rSK; bacterial; blood clot; thrombotic condition, myocardial infarction; venous thrombosis, pulmonary embolism; cerebral thrombosis; graft thrombosis; arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                         Recombinant streptokinase rSK59-414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 35; Page 65-66; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-terminally deleted streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR12892 standard; Protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                       97US-0069497
                                                                                                                                                                                                                                                                                                                                                           98WO-US26694
(first entry)
                                                                                                                                                                                                  Streptococcus equisimilis
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-395183/33
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99 SVDVEY 104
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                                                                                                                                                                                                                                                                 WO9931247-A1
                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998;
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26-AUG-1999
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17-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Gaps

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Best Loc Matches

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RESULT 17
AAR12892
ID AAR128
XX
AC AAR128
DT 25-MAJ
DT 17-SEJ

Gaps

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256 and 257. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AAQ10230, AAR10195-6 and AAR10198-R10200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-lys 414) and retaining streptokinase activity. One or more of the amino acids can be replaced by a different amino acid at the same position or it can be deleted Alternatively, an extra residue can be inserted into the sequence. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in Secondary and ARR10195-R10199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
                                                                                                                       Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 372;
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                    streptokinase; thrombolytic agent; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ono K, Sakata Y, Uenoyama
                                                                                                                     100.0%; Score 30; DB 12; 100.0%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 30; DB 12;
100.0%; Pred. No. 68;
cive 0; Mismatches 0;
                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                AAR10200 standard; Protein; 372 AA
                                                                                                                                                                                                                                                                                                                                                                        Streptokinase (1-372) derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 59; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90JP-0096830.
89JP-0179432.
89JP-0307957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90EP-0113099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SAKA ) OTSUKA PHARM FACTOR
                                                                                                                                    Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                           157 SVDVEY 162
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                                                                                        372 AA;
                                                                                                                                                                              1 SVDVEY 6
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11-JUL-1989;
27-NOV-1989;
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                                                                                          Sequence
                                                                                                                    Query Match
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                                                                                                                                                           Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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373-Lys 414) and Gln being substituted for Lys at both positions
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                                                                                                     Uenoyama T;
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                                                                                                     Sakata Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR10197 standard; Protein; 372 AA
                                                                                                                                                                                                     Claim 8; Page 59; 76pp; English.
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             90JP-0096830.
89JP-0179432.
89JP-0307957.
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89JP-0179432.
89JP-0307957.
                                                                                                     Ono K,
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                                                                     (SAKA ) OTSUKA PHARM FACTOR
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                                                                                                 Ogino K,
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                                                                                                                                WPI; 1991-016179/03
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Sequence 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVDVEY 6
                            11-JUL-1989;
27-NOV-1989;
               11-APR-1990;
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11-JUL-1989;
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                                                                                                   Majima E,
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LD AAR:
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Streptokinase derivative having a C-terminal deletion (i.e. Pro 373-Lyg 414) and Pro residues being inserted next to Lyg at both positions 256 and 257. Derivatives show a decreased antigenicity, higher stability in blood and greater selectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in patients with lung thrombus or myocardial infarction. See also AQ10230, AAR10195-7 and AAR10199-R10200.
                                                                                                                                                                                                                                                                                     Synthetic gene encoding streptokinase - scale, high purity prodn.
of streptokinase used as a thrombolytic agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 30; DB 12; Length 374; 100.0%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptokinase, SKC-2; plasminogen, plasmin; antigenicity; plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
            streptokinase; thrombolytic agent; myocardial infarction.
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                                                                                                                                                                                                                                  Sakata Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84007 standard; Protein; 384 AA.
                                                                                                                                                                                                                                                                                                                             Claim 10; Page 59; 76pp; English
                                                                                                                                                            89JP-0179432.
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                                                                                                                      90EP-0113099
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Best Local Similarity luv...
6, Conservative
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                                                                                                                                                                                                                                  Ogino K,
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                                                                                                                                                              11-JUL-1989;
27-NOV-1989;
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                                                                EP407942-A.
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                                      Synthetic
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                                                                                                                                           Streptokinase, SKC-2; plasminogen; plasmin; antigenicity; plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
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                                                                                                                 Amino acid sequence of a mutant streptokinase
                                                                                                                                                                                                                                                                                                                                                   (INGG-) CENT ING GENETICA & BIOTECNOLOGIA,
                                                                                                                                                                                                                                                                                                                                                                               Garcia Ojalvo A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 22-23; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY84006 standard; Protein; 372 AA.
                                                                                                                                                                                                                                                                                               99EP-0202639
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                                                                                      (first entry)
                                                                                                                                                                                                               Streptococcus equisimilis
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N-PSDB; AAZ99251.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or C-terminus
                                                                                                                                                                                                                                                                                               13-AUG-1999;
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                                                                                     03-JUL-2000
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                                                                                                                                                                                                 Synthetic
                                                             AAY84006,
       RESULT 21
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Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptokinase derivative having a C-terminal deletion (i.e. pro 373-Lys 414) and Arg 45 to Gly 68 also being deleted. In addition Gln residues replace Lys at positions 256 and 257. This is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic gene encoding streptokinase - scale, high purity prodn. of streptokinase used as a thrombolytic agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                              complications and other forms of thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                        Disclosure; Page 24-25; 54pp; English.
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89JP-0307957.
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Seralena Menendez A;
                              2000-226041/20
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                                                                                                                                                                                                                                                                                                                                                                           384 AA
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                            WPI; 2000-226041,
N-PSDB; AAZ99252
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                                                                                                          C-terminus
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27-NOV-1989;
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Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
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                                                                                                                                                                                                              Gaps
                                in blood and greater
 a combination of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating myocardial infarction, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
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                                                                                                                                                                            Length 391;
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example of a streptokinase derivative which is a comb individually claimed modifications. Derivatives show a decreased antiqenicity, higher stability in blaclectivity of thrombolytic activity and specificity. The protein is used as a thrombolytic agent in parlents with lung thrombus or myocardial infarction. See also AAQ10230, AAR10195-8 and AAR10200.
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                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 18-20; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                       AAY84004 standard; Protein; 401 AA.
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Seralena Menendez A;
                                                                                                                                                                                                                                                                                 134 SVDVEY 139
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                                                                                                                                          391 AA;
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                                                                                                                                                                                                                                                1 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                         AAY84004;
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                 RESULT 25
                                                                                                                                                                                                                                                                                                                                                 AAY84004
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KW Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS; KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia; KW hypothermia; brain; spinal cord; kidney; heart; lung; llver; skin; HIV; wiral disorder; hepatitis; retroviral; infection; encephalitis; FALS; meurodegenerative disorder; parkinson's disease; Alzheimer's disease; KW funtingcon's disease; cerebellar degeneration; cardiovascular disease; KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure; KW spetemic lupus erythematosus; insulin-dependent; diabetes mellitus; pernicious aneamia; dermatomyostis; enythema nodosum; myasthenia gravis; Syoren's syndrome; temporal arthritis; auti-phospholipilg syndrome; moplastic disorder; leukemia; blomerulonephritis; anti-phospholipilg syndrome; meplastic disorder; leukemia; sercoma; myeloma; carcinoma; neuroma; melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease; non-Hodgkin's lymbonary; macular degeneration; cataract; pernetical conticions; motor neuron disease; conticions; motor neuron disease; conticions; cervix; proceattion; cataract; conticions; disease; bypass surgery; charact; conticions; cervix; proceattion; cataract; conticions; cervix; conticis; motor neuron disease; conticions; cervix; proceattion; cataract; conticions; cervix; conticion; cataract; conticions; cervix; conticion; cataract; conticions; cervix; conticion; cataract; conticions; cervix; conticion; cervix; conticion; cataract; conticion; cervix; conticion; cervix; conticion; cervicions; cervicions
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                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides that ameliorate cell death useful for treating conditions associated with cellular differentiation
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                                                Indels
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                  Pred. No. 74;
Mismatches
                                                                                                                                                                                                                                                                                AAY25020 standard; peptide; 413 AA
100.08; F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                             6; Conservative
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                                                                                                                                (RABK/) RABKIN S W.
                     Best Local Similarity
                                                                                             1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1995;
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                                                Matches
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reperfusion injury, and hypertensive heart disease), immune disease (e.g. theumatoid arthritis, systemic lupus erythematosus, insulin-dependent, diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema nodosum, Sjogren's syndrome, temporal arthritis, myaathenia gravis, wegener's granulomatosis, glomerulomephritis, anti-phospholipid syndrome, and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia, arconas, myelomas, carcinomas, neuromana, cancers of the breast, brain, colon, cervix, and prostate, Hodgkin's disease and inflammatory induced cell damage to the eye, brain and other organs), ischemia or reperfusion injury (e.g. myocardial ischemia or reperfusion injury, renal ischemia, spinal cord ischemia and/or reperfusion injury, retinal ischemia, spinal cord ischemia and/or reperfusion injury, retinal ischemia, ordifarction, and stroke), toxic insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other organs from chemicals, radiation, pancreatitis, crohn's disease, ulcerative collits, accelerated aging, spinal cord disease (e.g. motor neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome chemically induced reperfusion, and therapeutics such as clozapine, AZT, and anthracyclines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present sequence represents a mutant protein of the streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garcia Ojalvo A, De La Fuente Garcia JDJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptokinase, SKC-2; plasminogen, plasmin; antigenicity, plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 30; DB 20; Length 413; 100.0%; Pred. No. 76; 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a mutant streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY84005 standard; Protein; 413 AA.
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus equisimilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seralena Menendez A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 SVDVEY 161
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                                                                                                                                                                                                                                                                                                                                                                                                          413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVDVEY 6
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streptokimase,

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Streptokinase; cell death; apoptosis; necrosis; nootropic;
neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;
antiinflammatory; antiarthritic; antichenmatic; cardiant;
M antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;
dermatological; antidiabetic; immunosuppressive; anti-HIV;
M dermatological; antidiabetic; immunosuppressive; ophthalmological;
M antiulcer; antibacterial; antiparasitic; neurodegenerative disease;
Parkinson's disease; haltheimer's disease; huntington's disease;
M cerebellar degeneration; neoplastic disease;
M catdiovascular disease; heart failure; atherosclerosis;
M mycoardial reperfusion injury; immune disease; autoimmune disease;
M mycoardial reperfusion injury; immune disease; autoimmune disease;
M systemic lupus erythematosus; diabetes mellitus; pernicious anemia;
M myelodegenerative diseases; viral diseases; macular degeneration;
M prion disease; aging.
                                                                                                                                                                                                                                                                                     ö
SKC-2. Streptokinase forms a complex with plasminogen, activating its conversion to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigenicity. The mutants are derived from the 1-1119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full-length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating myocardial infarction, pulmonary thromboembolism, surgical complications and other forms of thrombosis.
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                 100.0%; Score 30; DB 21; Length 413; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80012 standard; protein; 413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptokinase amino acid sequence.
                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                       144 SVDVEY 149
                                                                                                                                                                                                                413 AA
                                                                                                                                                                                                                                                                                                                     1 SVDVEY 6
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                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80012;
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 28
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The invention relates to an isolated peptide obtained from streptokinase, or its derivative or analog, which ameliorate cell death. The activity of peptides of the invention may be described as, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, cytostatic, antimiflammatory, antiparkinsonian, anticonvulsant, cytostatic, antimiflammatory, antiparkinsonian, anticonvulsant, cytostatic, cantiatheroselerotic, vasotropic, immunosuppressive, anti-HIV, dermatological, antidiabetic, antianaemic, virucide, ophthalmological, antidiabetic, antimanemic, virucide, ophthalmological, antidiabetic, antimanemic, virucide, ophthalmological, antidiabetic, antiparasitic. Peptides of the invention are useful for treating comprising peptides of the invention are useful for treating controlled of seases (e.g. harkinson's, Alzheimer's, Huntington's disease and cerebellar deseneration) neoplastic disorders including cancer, inflammatory disorders (e.g. arkinists, inflammatory joint disorders), cardiovascular diseases (e.g. heart failure, atheroselerosis and myocardial reperfusion injury), immune diseases (e.g. autoimmune confisease, acquired immunodeficiancy syndrome (ALDS), rheumatoid arthritis, systemic lupus erythematosus, diabetes mellitus, pernicious anaemia), myelodegenerative diseases, viral diseases, and degenerative diseases, uncerative, colitis, cataracte, pancreatitis, infectious diseases including bacteria, parasite, prion-based diseases, and ergenerative colitis, cataractes, and ergenerative sequence representative

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100.0%; Score 30; DB 23; Length 413; 100.0%; Pred. No. 76; 0; Indels (

Query Match Beet Local Similarity 100.vv Trahes 6; Conservative

156 SVDVEY 161

1 SVDVEY 6

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streptokinase amino acid sequence.

413 AA;

ABG74199 standard, Protein; 413 AA.

RESULT 29 ABG74199 06-MAY-2003 (first entry)

ABG74199;

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Representative streptokinase sequence.
                                                                              Unidentified,
                                                                                         Peptide
(MOLE-) MOLECULAR THERAPEUTICS INC.
                                                                 99US-0294457.
                                                                        95US-008233P.
96US-0759599.
                                                                                           Krystal G, Rabkin SW;
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US6348567-B1

Synthetic.

19-FEB-2002.

19-APR-1999; 06-DEC-1995; 05-DEC-1996; New peptides obtained from streptokinase, useful in ameliorating cell death due to apoptosis and/or necrosis and treating neurodegenerative, neoplastic, immune, cardiovascular and inflammatory disorders

WPI; 2002-266542/31.

Disclosure, Fig 3; 18pp; English

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Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS; Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma; atheroscienosis; myocardial infarction; immune disease; carcinoma; rheumatoid arthritis; mopplastic disorder; inflammatory disorder; arthritis; inflammatory induced cell damage; motor neuron disease; arthritis; inflammatory induced cell damage; motor neuron disease; physical insult; severe shock; ischaemia; reperfusion injury; hepatitis; cell dath associated procedure; spinal cord reperfusion injury; toxic insult, liver toxicity; pulmonary toxicity; spinal cord disease; Guillain-Bare syndrome; bypass surgery; myocardial ischaemia; chemotherapp; viral disease; viral encephalitis; infectious disease; bacterial disease; prion-based disease; macular degeneration; cataract formation; pancreatitis; Crohn's disease; ulcerative colitis; accelerated aging; oxidative stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= 18mer_peptide
/note= "Cell death ameliorating peptide. Specifically
claimed in claim 2. This is SEQ ID NO 5 as shown
in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Cell death ameliorating peptide. Specifically claimed in claim 2"
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/label= 6mer_peptide_#1
/note= "Cell_death_ameli
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/label= 18mer_peptide
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1 SVDVEY 6

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The invention relates to a pharmaceutical composition, which comprises a peptide capable of ameliorating cell death, its derivative or analogue, comprising a sequence Val-App-Val, where the peptide is in a suitable pharmaceutical carrier or dibuent. The pharmaceutical composition (comprising the peptide) is useful for treating or preventing cell death associated with a neurodegenerative disorder e.g. Parkinson's disease and Alzheimer's disease; cardiovascular disease e.g. AIDS and therosclerosis and myocardial infarction; immune disease e.g. AIDS and creumatory disorder e.g. arthritis and inflammatory induced cell camage; inflammatory disorder e.g. arthritis and inflammatory induced cell camage; disease caused by physical insult e.g. trauma and severe shock; inflammatory disorder e.g. arthritis and inflammatory induced cell camage; disease caused by physical insult e.g. trauma and severe shock; is chaemia or reperfusion injury e.g. myocardial ischaemia and spinal cord creperfusion injury; toxic insult e.g. inver toxicity and pulmonary toxicity; spinal cord disease e.g. motor neuron disease and Guillain-Bare confencious diseases e.g. bepatitis and viral encephalitis; chematherapy; viral disease e.g. hepatitis and viral encephalitis; chematherapy; viral disease e.g. hepatitis and viral encephalitis; confencious diseases e.g. becterial disease and prion-based disease; macular degeneration; cataract formation; pancreatitis; Crohn's disease; macular degeneration; cataract formation; pancreatitis; Crohn's disease. C. demochemal. The present sequence represents the amino acid sequence of a representative colitis; accelerated aging and oxidative stress in a warm-colocoded animal. The present sequence represents the amino acid sequence core peptides are produced.
/note= "Cell death ameliorating peptide. Specifically claimed in claim 2. This is SEQ ID NO 5 as shown on page 8"
                                                           156..176 Fraction 13 peptide
//label= Fraction 13 peptide
/note= "Cell death ameliorating peptide. Specifically
                                                                                                                                                                                                                                                                                                           299..318
/label= Fraction 12 peptide
/note= "Cell death ameliorating peptide. Specifically
dialimed in claim 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pharmaceutical composition for treating e.g. neurodegenerative disorder, cardiovascular disease, neoplastic disorder, viral disease and immune diseases, comprises a peptide capable of ameliorating cell
                                                                                                                                                                  /label= 6mer_peptide #2
/note= "Cell_death ameliorating peptide. Specifically
claimed in claim 2"
                                                                                                                                                                                                                                               /label= 11mer peptide
/note= "Cell death ameliorating peptide. Specifically
claimed in claim 2"
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99US-0294457.
96US-0759599.
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                                                                                                                                             299..304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KRYS/) KRYSTAL G.
(RABK/) RABKIN S W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 AA;
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19-APR-1999;
05-DEC-1996;
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                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                        Synthetic gene encoding streptokinase - scale, high purity prodn of streptokinase used as a thrombolytic agent
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                                                                                                                                                                                                                                                                                                                                                                                        Streptokinase and its derivatives can be produced in large quantities with high purity for use as thrombolytic agents in patients with lung thrombus or myocardial infarction. See also AAR10195-R10200
                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptokinase; thrombolytic agent; myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasminogen activator; coronary thrombosis; ATCC-9542.
                                                                                                                                                                                                                                                                                         Uenoyama T;
                                                                                                          Streptokinase encoded by synthetic gene
                                                                                                                                                                                                                                                                                        Ono K, Sakata Y,
                                                  AAR10194 standard; Protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR20202 standard; Protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 51; 76pp; English.
                                                                                                                                                                                                                              90JP-0096830.
89JP-0179432.
                                                                                                                                                                                                            90EP-0113099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.equisimilis streptokinase.
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                                                                                                                                                                                                                                                                    (SAKA ) OTSUKA PHARM FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                        Majima E, Ogino K,
                                                                                                                                                                                                                                                                                                           WPI; 1991-016179/03
156 SVDVEY 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          414 AA;
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                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ10230
                                                                                                                                                                                                           09-JUL-1990;
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                                                                                      28-MAR-1991
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21-APR-1992
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                                                                                                                                                                    EP407942-A.
                                                                                                                                                  Synthetic.
                                                                   AAR10194;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR20202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 31
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Gaps

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100.0%; Score 30; DB 24; Length 413; 100.0%; Pred. No. 76; cive 0; Mismatches 0; Indels (

Conservative

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Claim 30; Page 60-61; 73pp; English
          93WO-US09502.
                             92US-0956692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE
                                                                                                          WPI; 1994-135561/16.
                                                                                                                                                                                                                                                                                                                                           SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-395183/33
                                                                                                                                                                                                                                                              414 AA;
                                                                                                                                                                                                                                                                                                                        1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX80492
         05-OCT-1993;
                            05-OCT-1992;
                                       29-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9931247-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1999.
                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                           157
                                                                                                                                                                                                                                                                                                                                                                                                               AAY24794;
                                                                                                                                                                                                                                                                                Query Match
                                                                                       Reed GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed GL;
                                                                                                                                                                                                                                                                                                                                                                         RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                 AAY24794
ID AAY
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                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                              The SKC-2 gene was isolated from S.equisimilis type C by gene amplification from the synthetic primers SK1, SK2 and SK3 (see AAQ20666-8). The SKC-2 gene was inserted into yeast expression vector PBS-7 for extracellular expression of streptokinase and into pNAO for intracellular expression in yeast. For expression in bacteria, the SKC-2 gene was inserted in plasmid pEKG3, between a trp promoter and a T4 terminator.
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                      Streptokinase C-2 gene from S.equisimilis type C - plasmids and transformants for large scale intra- and extracellular expression of SKC-2 useful in thrombolytic agents
                                                                                   Hidalgo AP, Doce RS, Marrero LFH;
Munoz BAM, Martinez WB, Somavilla MC;
Martinez LSH;
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                            100.0%; Score 30; DB 13; Length 414; 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptokinase; SK; Streptococcus equisimilis; plasminogen;
                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                (INGG-) CENT ING GENETICA & BIOTECNOLOGIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "claim 1, see CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "claim 3, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR63120 standard; protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244..352
/note= "claim 2, 11..352
                                                                                                                                                                                               Claim 13; Page 14; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "claim 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120..352
/note= "claim 3,
                         91AU-0078101.
                                             90CU-0000090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                   Chaplen RR,
Ramirez AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus equisimilis.
                                                                                                       Garcia J,
                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244..414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14..414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
                                                                                                                          WPI; 1992-024716/04.
                                                                                                                                                                                                                                                                                                                                                                                   SVDVEY 162
                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                          414 AA;
                                                                                                                                                                                                                                                                                                                                                                    1 SVDVEY 6
                                                                                                                                    N-PSDB; AAQ20665
                                                                                Garcia MPE, Cha
Collazo PR, Rar
Fernandez AP, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptokinase
                        31-MAY-1991;
                                             23-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9407992-A1,
       28-NOV-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
16-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1994
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                       157
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR63120;
                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising a sequence encoding amino acids 14-414 of streptokinase, which binds to plasminogen and does not have a sequence comprising amino acids 60-414 is new. The polypeptide pref. comprises amino acids 244-352, 1-352, 120-352 or 244-414.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Length 414;
                                                                                                                                                                                                                                                                           DNA encoding a polypeptide which binds to plasminogen and corresponds to region of streptokinase - useful to detect plasminogen in a sample and to treat myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus equisimilis native streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 30; DB
100.0%; Pred. No. 76;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 40-41; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY24794 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-terminally deleted streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%;
Matches 6; Conservative 0
93US-0128299,
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                                                      (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus equisimilis
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indepression to the control of an activation in a pharmaceutical composition comprising alloaded clots. Also described are: (1) a composition comprising an isolated modified streptokinase, the composition comprising an isolated modified streptokinase, the modification being removal of amino acid residues in the amino terminus; (2) a method for dissolving a blood clot in a subject, comprising administering to the subject a fibrin-dependent streptokinase; (3) an expression vector comprising (1); and (4) a host cell transformed with the expression vector comprising (1); and (4) a host cell transformed with the expression vector of (3). The pharmaceutical composition comprising a bacterial fibrin-dependent plasminogen activator; is useful for dissolving blood clots in patients with a thrombotic condition, e.g. myocardial infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis, graft thrombosis and arterial thrombosis. The modified streptokinase can also be used in non-human mammals. Streptokinase can also be used in non-human mammals. Streptokinase condition of plasminogen is at least 10-fold, preferably 100-fold graeter in the presence of fibrin than in the absence of fibrin. The modified streptokinase has at least none amino acid substitution that intendification classified streptokinase has at least none amino acid substitution that intendificated represents native streptokinase at least two-fold. The present contended to the streptokinase at least two-fold. The present contended to the streptokinase at least two-fold. The present contended to the streptokinase at least two-fold. The present contended to the streptokinase at least two-fold. The present contended to the streptokinase at least two-fold. The present contended to the streptokinase at least two-fold.
    present invention describes an isolated bacterial protein that
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Sequence

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0
100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76; ive 0; Mismatches 0; Indels
             Local Similarity 100.
nes 6; Conservative
                                                                    SVDVEY 162
                                                   1 SVDVEY 6
                                                                           157
 Query Match
                       Matches
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Gaps

AAY01556 standard; peptide; 414 AA. AAY01556; Native streptokinase protein sequence.

18-JUN-1999 (first entry)

Antigenic peptide, streptokinase, streptokinase-specific antibody, thrombolytic activity, thrombolytic therapy, glomerulonephritis, rheumatic fever

Streptococcus equisimilis

WO9908698-A1

25-FEB-1999.

98WO-US17114 18-AUG-1998;

97US-0055911 18-AUG-1997;

(GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.

Parhami-Seren B, Reed GL;

WPI; 1999-190113/16.

New polypeptides which bind streptokinase-specific antibodies useful in thrombolytic therapy Disclosure, Page 12, 44pp, English.

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The present sequence represents a native streptokinase. The specification describes a polypeptide which binds to a streptokinase-specific antibody and prevents the antibody binding to native streptokinase. The specification also
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                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus equisimilis H46A, streptokinase, mutant, fibrinolytic, plasma clot, hydrolysis, haemolytic Streptococcus, plasminogen, plannin, serine procease, fibrin, blood clot, thrombolytic, vascular thromboembolytic symptom, acute myocardial infarction,
describes a synthetic polypeptide (P1) comprising an epitope which binds to an streptokinase-specific antibody and reduces thrombolytic activity of streptokinase. P1 is used in thrombolytic therapy, and to prevent or treat glomerulonephritis and rheumatic
                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptokinase polypeptide - useful as plasmin-resistant
                                                                                                                           20; Length 414;
                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus equisimilis native streptokinase.
                                                                                                                          Score 30; DB;
Pred. No. 76;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by ACC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Column 7-10; 17pp; English.
                                                                                                                                                                                                                                                                                                   AAW94664 standard; Protein; 414 AA.
                                                                                                                        100.0%; Sc
100.0%; Pr
ive 0;
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                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibrinolysis; resistance.
                                                                                                                                                          6; Conservative
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                                                                                                                                                                                                                     157 SVDVEY 162
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                                                                                                                      Query Match
Best Local Similarity
                                                                                            414 AA;
                                                                                                                                                                                       1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5876999-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-1999
                                                                                                                                                                                                                                                                                                                                  AAW94664;
                                                                                              Seguence
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Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunogl bulin; therapeutic; streptokinase.

Streptococcus equisimilis.

WO9852976-A1.

98GB-0007751. 97GB-0010480. 97GB-0016197. 97GB-0025270. 97US-0067235.

14-APR-1998; 21-MAY-1997; 31-JUL-1997; 28-NOV-1997;

02-DEC-1997;

(BIOV-) BIOVATION LTD

WPI; 1999-045301/04.

Carr FJ;

98WO-GB01473

21-MAY-1998;

26-NOV-1998

Streptokinase (SK) protein sequence.

03-MAR-1999

AAW86143;

AAW86143 standard; Protein; 414 AA

AAW86143

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The present invention describes a mutant streptokinase (SK) polypeptide in which at least one of the amino acids in the ProS8-Lys59-Ser60-Lys61 segment of the corresponding native SK is replaced by another amino acid. The present sequence is mutant SK K195E. SK is a secretory protein of haemolytic Streptococcus able to activate human plasminogen (HPlg) to plasmin (HPlm), which is a serine protease able to catalyse the hydrolygis of fibrin in blood clots. The SK is useful as a thrombolytic agent in the treatment of vascular thromboembolytic symptoms such as acute myocardial infarction. Compared with wild-type SK, the K59E mutant is more resistant to degradation by human plasmin and is more effective both in acting as a fibrolytic agent and in activating human plasminogen.
                                                 Gaps
                                                                                                                                                                                                                                                                                                         Streptococcus equisimilis H46A, streptokinase, mutant, fibrinolytic; plasma clot, hydrolysis, haemolytic Streptococcus, plasminogen, plasmi, serine protease, fibrin, blood clot, thrombolytic; vascular thromboembolytic symptom, acute myocardial infarction; fibrinolysis; resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant streptokinase polypeptide - useful as plasmin-resistant thrombolytic agent
                100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                 Streptococcus equisimilis mutant streptokinase K59E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encoded by ACC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                       AAW94665 standard; Protein; 414 AA.
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Query Match
Beet Local Similarity 100.0.
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                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus equisimilis
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Best Local Similarity 100.
Matches 6; Conservative
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N-PSDB; AAX16633.
                                                                                                          SVDVEY 162
                                                                             1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                     AAW94665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu H;
                                                                                                                                                        RESULT 36
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The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein, (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of the SK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 100.0%; Score 30; DB 20; Local Similarity 100.0%; Pred. No. 76; es 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW86144 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Fig 28; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVDVEY 6
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AAW86144
ID AAW86:
XX
AC AAW86:
XX
DT 03-MA:
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Matches
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Gaps

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100.0%; Score 30; DB 20; Length 414; 100.0%; Pred. No. 76; ive 0; Mismatches 0; Indels 0

|||||| SVDVEY 162

157 Н

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SVDVEY

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Sundaram V;

Rajogopal K, Nihalani D,

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This sequence represents the human Streptococcus equisimilus streptokinase protein sequence. The invention relates to a hybrid plasminogen activator (PA) comprises a polypeptide fusion between plasminogen activator (PA) comprises a polypeptide fusion between careful activation are apable of plasminogen (FG) activation, and fibrin binding and so or land 2. The hybrid PA possesses the ballity to bind with fibrin independently and also characteristically retains a PG activation ability which becomes evident only after a pronounced duration, or lag, after exposure of the PA to a suitable and pronounced duration, or lag, after exposure of the PA to a suitable candious are useful in thrombolytic therapy for various kinds of cardiovascular disorders. The hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptokinase in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into the vascular system without significantly activating the circulating blood plasminogen activation thous aiding in the call activation of the plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation cencountered during clinical use of streptokinase.
                                                                                                                                                                                                                                                                                                                                                               Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding domains of human fibronectin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 21; Length 414; 100.0%; Pred. No. 76; 0; Indels ()
                                                                                                                                                                                (COUL ) CSIR COUNCIL SCI IND RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 3; 58pp; English
                                                                                         99EP-0310541
                                                                                                                                      98IN-0003825
                                                                                                                                                                                                                               Kumar R, Roy C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                 2000-516032/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 AA;
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                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA37633
EP1024192-A2
                                                                                         23-DEC-1999;
                                                                                                                                      24-DEC-1998;
                                            02-AUG-2000,
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                                                                                                                                                                                                                             Sahni G,
Yadav M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins. The method comprises determining at least part of the amino acid sequence of the protein; (b) identifying in the amino acid sequence one or more potential epitopes for T-cell epitopes) of the given species, and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immunogenicity of the protein when exposed to the immuno species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic protein? Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of a de-immunised SK protein molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to a method for the production of non-immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptokinase; SK; hybrid plasminogen activator; fibrin binding region; plasminogen; human; fibronectin; thrombolytic therapy; cardiovascular disorder; fibronectin.
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                                                          Non-immunogenic, epitope, T-cell; immunogenicity; immune system; SK;
immunogl bulin; therapeutic; streptokinase; de-immunised.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
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Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels
                De-immunised streptokinase (SK) protein sequence
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97GB-0010480.
97GB-0016197.
97GB-0025270.
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                                                                                                                               Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOV-) BIOVATION LTD
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                                                                                                                                                                         WO9852976-A1
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31-JUL-1997;
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Carr FJ;

Sequence

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Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug; vaccine; carrier; diagnosis; therapy; complement; C3; C5; CVF; plasminogen; streptokinase; fibrin; blood clot; thrombolysis; plasmin; myocardial infarction.
                                                                                      Wild type streptokinase from Streptococcus equisimilis.
AAB01295 standard; protein; 414 AA.
                                                                                                                                                                                             Streptococcus equisimilis.
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Gaps

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0; Indels

Carter

Hamilton AA,

99WO-GB04119 98GB-0026925 99GB-0002139

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plasmin; myocardial infarction.
                                                                 Streptococcus equisimilis
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                                                                                                                                                                                                                                                                                                                                   Carr FJ, Adair FS,
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-423372/36.
                                                                                                       WO200034317-A2
                                                                                                                                                                                                                           08-DEC-1998;
02-FEB-1999;
                                                                                                                                                                                     08-DEC-1999;
                                                                                                                                               15-JUN-2000
                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB74940
    %$GGGGGGGGGGGGGGGGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                   Proteins or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at least one of these T cell epitopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for the immunogenic within an enzymatic activity which has a beneficial therapeutic effect, a protein used to convert inactive drugs to its active form within a living organism. The method can be used so a carrier of other molecule or a protein which binds to other molecules or carrier of other molecules within or introduced within the living organism in order to alter the bio distribution of other molecules, such that the protein does not strinulate immune response in the living organism. The less immunogenic protein is useful in medicine, diagnosis and in manufacture of a certain strains of beta-haemolytic streptococi: The protein has no certain strains of beta-haemolytic streptococi: The protein has no certain strains of beta-haemolytic streptococi: The protein has no certain strains of beta-haemolytic streptococi: Streptokinase is considerable clinical importance owing to its ability to efficiently bind human plasminogen, considerable clinical importance of fibrin filaments in blood clots. Streptokinase is an effective thrombolytic agent in the treatment of coronary thrombosis, myocardial infarction. The native protein is immunogenic and the protein to a single use. The netwood protein a longer correptokinase. The streptokinase sequence of the wild type streptokinase. The streptokinase sequence is given in AAB01296. See GENESEQ records AAB01289-B01302.
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                                                                                                                                                                                                                                                                                                     Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes
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vaccine; carrier; diagnosis; therapy; complement; C3; C5; CVF;
plasminogen; streptokinase; fibrin; blood clot; thrombolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Altered streptokinase from Streptococcus equisimilis.
                                                                                                                                                                                                                       Hamilton AA, Carter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB01296 standard; protein; 414 AA.
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                                                                            99WO-GB04119
                                                                                                                    98GB-0026925.
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                                                                                                                                                                               (BIOV-) BIOVATION LTD.
                                                                                                                                                                                                                         Carr FJ, Adair FS,
                                                                                                                                                                                                                                                               WPI; 2000-423372/36.
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WO200034317-A2
                                                                                                                    08-DEC-1998;
02-FEB-1999;
                                                                              08-DEC-1999;
                                      15-JUN-2000
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Proteins or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at lesst one of these T cell epitopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for producing a protein with an enzymatic activity which has a beneficial therapeutic effect, a protein used to convert inactive duugs to its active form within a living organism, a vaccine, a protein used as a carrier of other molecule or a protein which binds to other molecules within the living organism in order to alter the bio distribution of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic protein is useful in medicine, diagnosis and in manufacture of a timulate immune response in the living organism. The less immunogenic protein is useful in medicine, diagnosis and in manufacture of a certain strains of beca-haemolytic streptochiase is produced by contracting its activity but has considerable clinical importance of insolution of fibrin filaments in blood clots. Streptokinase is an dissolution of fibrin filaments in blood clots. Streptokinase is an effective thrombolytic agent in the treatment of coronary thrombosis, improving survival and preserving left ventricular function following production of neutralising antibodies in humans generally limits the correct or a simple was man man manufacture of a longer or more in the manufacture of a longer or more in the manufacture of a longer or more in the limit and manufacture of a longer or more in the limit and manufacture or and manufacture or and
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Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes
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is given in AAB01295. See GENESEQ records AAB01289-B01302.
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                                                                                                                                                                                                Example 2; Fig 6; 42pp; English.
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Best Local Similarity 100.0%
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Sequence

Query Match Matches 157

g

AAB01296;

Streptococcus plasminogen activator, streptokinase Plasminogen activator; cardiant; thrombolytic; heart attack; stroke; blood clotting disorder.

Streptococcus sp. WO200032759-A1.

(first entry)

13-SEP-2000

AAY99593;

(OKLA-) OKLAHOMA MEDICAL RES FOUND.

02-DEC-1998; 06-MAY-1999;

99WO-US09991. 98US-0110588.

08-JUN-2000.

AAY99593 standard; protein; 415 AA.

43 AAY99593

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The present invention describes a method to create mutants of streptokinase (SK) which become more resistant to hydrolytic inactivation by human plasmin (HPIM) and more effective in activation of chuman plasmin (HPIM) and more effective in activation of chuman plasmin (HPIM) than the native SK that is commercially available. The novel HPIM hydrolysis resistant SK can be created by the near the peptide bonds that are hydrolysed by HPIM. The mutant SK can be used to form HPID and native SK and could be used as a thrombolytic agent. The mutant SK sequence could be coupled with other proteins to form fusion proteins and improve the fibrinolytic activity of the fusion proteins. Some truncated SKs such as SKIG-378) could activate HPIG as efficiently as native SK. The truncated SKs comprising the modification of ProS8-LysSS-Ser60-Lys61 to other amino acids would have a better thrombolytic activity than the corresponding native truncated SK. Since LysS9-Ser60 is among the few peptide bonds which are cleaved in the early reaction with HPIM and the MR2-terminal peptide chain of 11e1-LysS9 is essential in stabilising the structure of SK, the mutation at for near by the peptide bond and might improve the stability of the hydrolysis of the peptide bond and might improve the stability of streptokinase (KS9E) given in the present sequence represents the mutant streptokinase (KS9E) given in the present invention.

N.B. The present sequence corresponds to the indexers best interpretation of thin print.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of novel streptokinase mutants as improved thrombolytic
                                                                                                                                                                                                                         Misc-difference 370
/label= unknown
/note= "given as being encoded by NNN due to poor
quality text"
                                                                                                                                                                                                      /note= "given as being encoded by NNN due to poor
quality text"
                                    Streptokinase, mutant, human, plasmin; plasminogen, thrombolytic.
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Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels (
                                                                                                                                             note= "Lys in wild type sequence"
Mutant streptokinase protein sequence K59E.
                                                                                                          Location/Qualifiers
                                                                                                                                                                                    'label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 1; 4pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     95TW-0107238.
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                                                                                                                                                                   Misc-difference 127
                                                                                                                                Misc-difference 59
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                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agents
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The present sequence is streptokinase, a single-peptide secretory protein which is produced by various strains of haemolytic Streptococcus. Streptokinase forms a tight binding complex with human plasminogen, causing the spontaneous conversion of plasminogen to its active form, plasmin. Plasminogen is the principal serine protease zymogen in the extracellular fluids of vertebrates. Plasmin is implicated in pericellular proteolysis associated with a wide range of physiological and pathological processes. Plasminogen activators regulate plasminogen expression either by forming a binding complex, as in the case of streptokinase, or by hydrolysing a peptide bond in plasminogen to convert it to plasmin. Review of sequence homologies of several plasminogen citrators and chymotrypsin has identified a six amino acid peptide in citrators and chymotrypsin has identified is particularly useful when inserted between amino acid residues 644 and 645 of full length chuman plasminogen. Novel plasminogen activators have been made based upon chuman plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preparing thrombolytic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the plasminogen activation/recognition site of plasminogen binding proteins. The polypeptides are useful in preparing thresholvers and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 30; DB 21; Length 415; 100.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or treating blood clotting disorders such as heart attack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 29-31; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY50870 standard; protein; 415 AA.
                                                                                                                                                                                                                                                                                                                                                                                            Zhang XC, Tang JJN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-422975/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY50870;
                                                                                                                                                                                                                                                                                                                                                                                            Lin X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 44
AAY50870
ID AAY50
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AC AAY50
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157 SVDVEY 162

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1 SVDVEY 6

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Streptokinase produced using E.coli transformed with a recombinant streptokinase vector can be isolated for use as a thrombolytic agent to facilitate the in vivo lysis or dissolution of blood clots. The vector is esp. a plasmid obtd. from E.coli, esp. plasmid pBR 322. Recombinant plasmid pMF1 as defined by a restriction endonuclease map is claimed. Escherichia coli HB 101 harbouring plasmid pMF1 is deposited as ATCC 39613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptokinase A; recombinant phage; thrombolytic agent; plasminogen;
                                                                                                                                                                                                                                                                                                                                                                       Streptokinase prodn. - by cultivating Escherichia coli ATCC 39613 contg. recombinant plasmid pMF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High yield streptokinase A prodn. from infected bacteria - contg. recombinant phage including gene from Streptococcus, useful as thrombolytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 30; DB 6; Length 440; 100.0%; Pred. No. 82; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptokinase A from Streptococcus pyogenes SF130/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR06378 standard; protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DEAK ) AKAD WISSENSCHAFTEN DDR.
                                                                                                                                        (PHIP ) PHILLIPS PETROLEUM CO. (UYOK-) UNIV OF OKLAHOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example, Fig 2; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 2; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malke H;
                          84US-0585417.
83DD-0255523.
83DD-0255235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88DD-0321532,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88DD-0321532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
                                                                                                                                                                                                                               Malke H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (nbdated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walter F, Siegel M,
                                                                                                                                                                                                                                                                                       WPI; 1985-135032/23.
N-PSDB; AAN50493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 SVDVEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-247328/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVDVEY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ05604.
                          02-MAR-1984;
10-OCT-1983;
10-OCT-1983;
                                                                                                                                                                                                                                  Perretti JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
20-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD276694-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR06378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 46
AAR06378
AC AAR0
XX AAR0
DT 20-D
XX STRE
XX SIRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel thrombolytic agent comprising streptokinase where at least one nonessential portion has been modified. The invention also describes a method of forming a thrombolytic agent comprising determining a nonessential portion of streptokinase and modifying the nonessential portion to render the resulting protein less antigenic. The modified streptokinase is used to treat blood clot disorders, such as heart attacks. The modified streptokinase has less antigenicity than streptokinase but is still able to complex plasminogen and lead to plasminogen activation. Modified streptokinase with the smaller proteins are cheaper and easier to produce. This sequence represents a fragment of a Streptococcus sp. streptokinase protein which is used in the description of the method of the invention.
                                                                                                              Thrombolytic agent; streptokinase; antigenic; blood clot; heart attack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New thrombolytic agents derived from modified humanized streptokinase, useful for treating blood clot disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 30; DB 21; Length 415; 100.0%; Pred. No. 77; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoded by skc streptokinase gene on the 2.5kb PstI produced pMF1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ົວ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus equisimilis strain H46A (serological group
                                                        Streptococcus sp. streptokinase protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzyme; thrombolytic agent; blood clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 48-49; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP50620 standard; Protein; 440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0084392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lin X, Tang JJN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84AU-0033859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.vv
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-052966/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVDVEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVDVEY 6
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                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                      W09957251-A2.
                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-0CT-1984;
24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-1991
                                                                                                                                                                                                                                                                                                               11-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang XC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157
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Matches 6; Conserv
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        Lambda L47.1 is ligated with genomic DNA from S. pyogenes SF130/13 and the resultant product used to transform bacteria. Infected cells are cultured in liq. medium contga assimilable C and N sources, and streptokinase A is isolated from the cell lysate. The infected cells provide the protein in high yields, i.e. 1000 U/ml compared to 80 U/m; for the donor strain. The protein activates the autocatalytic conversion of human plasmin, so is potentially useful as a thronbolytic agent. See also DD 276693 (AAQ05603).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pMW1 (contg. the streptokinase G gene ) is ligated with pUC19 and the resultant product used to transform bacteria. Infected cells are cultured in 1iq. medium contg. assimilable C and N sources, and streptokinase G is isolated from the cell lysate.

The infected cells provide the protein in high yields, i.e. 600 U/ml which is 1.5-2 times that for the donor strain. The protein activates the autocatalytic conversion of human plasmin, so is potentially useful as a thronbolytic agent. See also DD-276634 (AAQ05664).

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High yield streptokinase G prodn. from recombinant cells -
transformed with plasmid contg. gene from Streptococcus, useful
as thrombolytic agent
                                                                                                                                                                      .
0
                                                                                                                                                100.0%; Score 30; DB 11; Length 440; 100.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                            Streptokinase G protein from Streptococcus pyogenes G19908.
                                                                                                                                                                                                                                                                                                                                                              Streptokinase G; thrombolytic agent; plasminogen; plasmin;
                                                                                                                                                                     Indela
                                                                                                                                                                     ..
                                                                                                 agent. See also DD-276693 (AAQUS603).
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                   AAR06377 standard; protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DEAK ) AKAD WISSENSCHAFTEN DDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malke H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             88DD-0321531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88DD-0321531.
                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Siegel M,
                                                                                                                                                                                                                                                                                                                                                                           recombinant plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-247327/33.
                                                                                                                                                                                                               183 SVDVEY 188
                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                            440 AA;
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                                                                                                                                                                                          1 SVDVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-1988;
                                                                                                                                                                                                                                                                                                          25-MAR-2003
20-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                  DD276693-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walter F,
                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                        AAR06377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                              RESULT 47
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The sequence was deduced from PCR amplified chromosomal DNA from S. equisimilis (Lancefield's Gp C ) Arcc 10009 or Arcc 9642. The primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]). See Swiss-Prot K02986 and P00779 and Geneseq N70106. The gene can be used to construct expression vectors in which the streptokinase gene is linked to a second gene encoding e.g. another streptokinase protein, hirdin, or a streptokinase-like protein, via a linking sequence encoding a cleavage site for e.g. factor Xa or thrombin. The enzymes which cleave the fusion protein are present at the site of the target thrombus so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the active agents are released specifically at the place where clot formation is occurring.
See also R12887, R12888, R12891-R12894, R12885 and R12522.
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 440;
82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus equisimilis ATCC 9542 or ATCC 100009
100.0%; Score 30; DB 11;
11arity 100.0%; Pred. No. 82;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27..440
/label= mature streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..26
/label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Czapleswski LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 80; 115pp; English
                                                                                                                                                                                                                                                                                                        AAR12889 standard; Protein; 440 AA
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-208151/28.
N-PSDB; AAQ12156.
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Best Local Similarity
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                                                                                                           1 SVDVBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptokinase.
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17-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                           AAR12889;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5481 sequences (31), given in the specification. The proteins have antibacterial and antiinflammatory activity. [1], nucleic acids encoding (1), ABN6604-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly 8. agalactiae and 8. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a streptococcus from ample: (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity contactors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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   0; Indels
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   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus polypeptide SEQ ID NO 8298.
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                                                                                                                                                                                                                                                                                                                  ABP29561 standard; Protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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   6; Conservative
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N-PSDB; ABN70192.
                                                                                                                                         183 SVDVEY 188
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                                                                        1 SVDVEY
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Tettelin H;
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ABRESOLT 49
AC ABRESOL
XX ABRESOL
XXX 02-JU
XXX Strep
XXX Strep
XXX Strep
XXX Strep
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The protein is a recombinant product of a gene fusion construct.

The sequence of the synthetic hirudin HV-1 genes was designed based on the published manno acid sequence (bodt J., et al FEBS Letters 165 180 (1984)). The sequence of streptokinase was obtd.

From PCR amplified chromosomal DNA from S. equisimilis ATCC 10009 or ATCC 9642. The primers used for the PCR were based on the published DNA sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti, J.J., Gene 34 357-362 [1985]). The two sequences were used to construct an expression vector in which the hirudin gene is linked to the streptokinase gene via a linking sequence encoding a cleavage site for factor Xa. The factor Xa is present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also AAR12887-R12889, AAR12891-R12894 and AAR12522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 30; DB 12; Length 483; Best Local Similarity 100.0%; Pred. No. 91; Matches 6; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                 Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis.
                                                                                                                                                                                                                                                                                                                                              66..69
/label= linker
/note= "factor Xa cleavage site"
                                                                                                                                                                                    Factor Xa-cleavable hirudin-IEGR-streptokinase.
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/label= streptokinase
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/label= hirudin HV-1
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                                                                           AAR12885 standard; Protein; 483 AA
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89GB-0027722.
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(first entry)
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 183 SVDVEY 188
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17-SEP-1991
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                                                                                                         AAR12885;
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Query Match
Best Local Similarity 100.
Matches 6; Conservative

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100.0%; Score 30; DB 23; Length 440; 100.0%; Pred. No. 82; cive 0; Mismatches 0; Indels

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Search completed: January 20, 2004, 13:56:15 Job time : 43 secs දු දු

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Sequence 1, Application US/09919703
Patent No. US20020165129A1
GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-919-703-1
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 5,
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1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCCMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-919-703-12
US-09-919-703-12
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US-10-300-215-252
US-10-300-215-252
US-10-369-493-687
US-10-369-493-6887
US-10-369-919-703-3
US-10-369-919-703-3
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US-10-193-886-12
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Sequence 25, Appliseduence 1185, Appliseduence 14, Appliseduence 15, Appliseduence 16, Appliseduence 16, Appliseduence 12, Appliseduence 12, Appliseduence 19042, Appliseduence 19042, Appliseduence 1049, Appliseduence 11170, Appliseduence 111710, Appliseduence 111710, Appliseduence 111710, Appliseduence 11170, Appliseduence 111710, Appliseduence 111710, Appliseduence 11170, Appliseduen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
TITLE REPERENCE: 50216/003004
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT PILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR PILING DATE: 1999-04-19
PRIOR PILING DATE: 1999-04-19
PRIOR PILING DATE: 1996-12-05
PRIOR FILING DATE: 1996-12-05
PRIOR FILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 16
SEQ I
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Patent No. US20020165129A1

GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/00304
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR PELING DATE: 1999-04-19
PRIOR PELING DATE: 1995-12-05
PRIOR PELING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 21
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Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide
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Patent No. US20020165129A1
GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 6; Conserv
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US-09-919-703-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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   TITLE OF INVENTION: Cell Death
CURRENT APPLICATION NUMBER: US/09/919,703
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 09/294,457
PRIOR PILING DATE: 1999-04-19
PRIOR PILING DATE: 1999-04-19
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SENGTH: 6
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Patent No. US20020165129A1
GENERAL INFORMATION:
APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conservative
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US-09-919-703-5
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Query Match

FEATURE:

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100.0%; Score 30; DB 12; Length 414; 100.0%; Pred. No. 95; tive 0; Mismatches 0; Indels (
                                                                            PUDLICATION:

GENERAL INFORMATION:

APPLICANT: CARR, Francis Joseph
APPLICANT: CARR, Francis Joseph
APPLICANT: ADAIR, Fiona Suzanne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: HAMILTON, Anita Anne
APPLICANT: CARTER, Graham
TITLE OF INVENTION: NON-IMMUNOGENIC FROTEINS
FILE REFERENCE: MER-104-Con.1
CURRENT FILING DATE: 1099-11-20
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-05-21
PRIOR FILING DATE: 1997-05-21
PRIOR FILING DATE: 1997-05-21
PRIOR FILING DATE: 1997-05-21
PRIOR PRILING DATE: 1997-05-21
PRIOR PRILING DATE: 1997-07-31
PRIOR APPLICATION NUMBER: GB 9716197.0
PRIOR PRILING DATE: 1997-07-31
PRIOR PRILING DATE: 1997-07-31
PRIOR PRILING DATE: 1998-04-14
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Publication No. US200301530431
GENERAL INFORMATION:
APPLICANT: CARA, Francis Joseph
APPLICANT: ADAIR, Fiona Suzanne
APPLICANT: AMAILTON, Anita Anne
APPLICANT: AMAILTON, Anita Anne
APPLICANT: AMAILTON; Anita Anne
APPLICANT: APPLICATION NUMBER: US/10/300,215
CURRENT FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 09/439,136
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1997-05-21
PRIOR PLILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-11-28
PRIOR FILING DATE: 1997-11-28
PRIOR FILING DATE: 1997-11-28
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1997-11-20
NUMBER OF SEQ ID NOS: 254
NUMBER OF SEQ ID NOS: 254
             Sequence 252, Application US/10300215
Publication No. US20030153043A1
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; ORGANISM: Streptococcus equisimilis
US-10-300-215-252
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Best Local Similarity 100.
Matches 6; Conservative
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US-10-300-215-253
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Publication No. US20030059921A1

GENERAL INDORMATION:
APPLICANT: Kumar, Rajesh
APPLICANT: Sahni, Girish
APPLICANT: Rajespal, Kammara
APPLICANT: Alagopal, Kammara
APPLICANT: Vacav, Mahavir
APPLICANT: Vacav, Mahavir
APPLICANT: Sundaram, Vasudha
APPLICANT: Wardy Mahavir
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Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: Peptides and Their Use to Ameliorate
TITLE OF INVENTION: Cell Death
FILE REFERENCE: 50216/003004
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US/09/919,703
PRIOR PAPLICATION NUMBER: US 09/294,457
PRIOR PAPLICATION NUMBER: US 08/759,599
PRIOR PAPLICATION NUMBER: US 08/759,599
PRIOR PAPLICATION NUMBER: US 08/759,599
PRIOR PAPLICATION NUMBER: US 06/008,233
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic polypeptide US-09-919-703-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-300-215-252
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LENGTH: 414
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Sequence 6887, Application US/10369493

Sequence 6887, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Blater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 6887

LENGTH: 629
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; Sequence 3, US20020165129A1
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
; APPLICANT: Rabkin, Simon W.
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate
; TITLE OF INVENTION: Cell Death
; FILE REFERENCE: S0216/003004
; CURRENT APPLICATION WUMBER: US/09/919,703
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 09/294,457
; PRIOR PLING DATE: 1999-04-19
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO : LENGTH: 6
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Pred. No. 4.2e+02;
2; Mismatches 0; Indels
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90.0%; Score 27; DB 10; 1
Best Local Similarity 83.3%; Pred. No. 6.7e+05;
Matches 5; Conservative 1; Mismatches 0;
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US-09-919-703-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.3%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                     170 SVDIEY 175
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                     1 SVDVEY 6
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// Sequence 5723, Application US/10369493

// Sequence 5723, Application US/10369493

// Sequence 5723, Application US/10369493

// Publication No. US20030233675A1

// Publication No. US20030233675A1

// APPLICANT: Cao, Yongwei

// APPLICANT: Hinkle, Gregory J.

// APPLICANT: Glodman, Barry S.

// APPLICANT: Chen, Xianfeng

// TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

// TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

// TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

// FILE REFERENCE: 38-10(52052)B

// CURRENT APPLICATION NUMBER: US 60/360,039

// PRIOR FILING DATE: 2002-02-21

// NUMBER OF SEQ ID NOS: 47374
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| Sequence 25, Application US/09862027
| Sequence 25, Application US/09862027
| Sequence 25, Application US/09862027
| Setent No. US2000142428A1
| APPLICANT: Hodge, Martin R.
| TITLE OF INVENTION: NO. US20020142428A1e1 Kinases and Uses Thereof
| FILE REFERENCE: 35800/234662
| CURRENT APPLICATION NUMBER: US/09/862,027
| CURRENT APPLICATION NUMBER: US 09/345,473
| PRIOR FILING DATE: 1999-06-30
| NUMBER OF SEQ ID NOS: 82
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 25
| LENGTH: 891
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                                                                                                                                                                                                   100.0%; Score 30; DB 12; Length 414; 100.0%; Pred. No. 95; 1.tive 0; Mismatches 0; Indels 0
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                                                                                                FEATURE:
, OTHER INFORMATION: Modified strep protein
US-10-300-215-253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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, ORGANISM: Hydra vulgaris
US-09-862-027-25
                                                                                                                                                                                                                                                                                                                                                            157 SVDVEY 162
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                           1 SVDVEY 6
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LENGTH: 1207
SEQ ID NO 253
LENGTH: 414
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Gaps
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Publication No. US20030008344A1
GENERAL INFORMATION:
APPLICANT: ADLER, JON ELLIOT
APPLICANT: ZOZULYA, SERGEY
APPLICANT: COCONNELL, STADONG
APPLICANT: COCONNELL, STADONG
APPLICANT: STASZEWSKI, LENA
TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
FILE REFERENCE: 070803/0277470/RXT
CURRENT APPLICATION NUMBER: US/09/799,629
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,546
PRIOR PLING DATE: 2000-03-07
PRIOR PLING DATE: 2000-03-07
PRIOR PLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,536
PRIOR PLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/209,840
PRIOR APPLICATION NUMBER: 60/209,840
PRIOR APPLICATION NUMBER: 60/209,840
PRIOR APPLICATION NUMBER: 60/209,840
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Sequence 12, Application US/10193896

Publication No. US20030129710A1

GENERAL INFORMATION:

APPLICANT: Bioteknologiek Institut

APPLICANT: Hansen, Plemming

APPLICANT: Stougaard, Peter

APPLICANT: Berthelsen, Plemming

APPLICANT: Brithaauer, Kaien

APPLICANT: Brithaauer, Karen

APPLICANT: Hansensen, Hans

TITLE OF INVENTION: hereof

TITLE OF INVENTION: hereof

TITLE OF INVENTION: hereof

CURRENT APPLICATION NUMBER: 06/305,108

PRIOR APPLICATION NUMBER: 06/305,108

PRIOR APPLICATION NUMBER: 09/905,108

PRIOR APPLICATION NUMBER: 09/905,108

PRIOR APPLICATION NUMBER: 09/905,108

PRIOR APPLICATION NUMBER: 09/905,108

PRIOR PILING DATE: 2001-07-16

MUMBER OF SEQ ID NOS: 14

SEQ ID NO 12

LENGTH: 496

MUMBER: DATE: DATE
                                                                                                                                                                 Score 27; DB 12; Length 391;
Pred. No. 4.2e+02;
1; Mismatches 0; Indels
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TYPE: PRT ORGANISM: Gallid herpesvirus 3
                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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451 AVDVEY 456
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US-10-193-896-12
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US-10-193-896-12
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US-09-799-629-14
                                                                                US-10-209-967-14
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| Sequence 14, Application No. US20030171279A1
| Sequence 14, Application No. US20030171279A1
| GENERAL INFORMATION:
| APPLICANT: MUNGER, JOSHUA
| APPLICANT: ROIZMAN, BERNARD
| TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND TITLE OF INVENTION: BAD-INVOLVED APOPTOSIS
| TITLE OF INVENTION: WHABER: US/10/209,967
| CURRENT APPLICATION NUMBER: US/202-07-31
| PRIOR PELLING DATE: 2001-07-31
| NUMBER OF SEQ ID NOS: 25
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                             APPLICANT: Haake, David A.

APPLICANT: Haake, David A.
Shang, Ellen S.
TITLE OF INVENTION: Leptospira MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/992,807
FILING DATE: 16-Jan-2002
CLASSIFICATION: ~UNKNOWN>
PRIOR APPLICATION: ~UNKNOWN>
ATTORNEY/AGENT INFORMATION:
**MANGER OF THE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WONG, Wean Khing
REGISTRATION NUMBER: 33,561
REFRENCE/DOCKET NUMBER: 5656-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-992-807-6
                                                                                                                                                                                                         ; Sequence 6, Application US/09992807; Patent No. US20020127240A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
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Best Local Similarity 83.3
Matches 5; Conservative
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23 TVDVEY 28
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1 TVDVEY 6
                                                                                                                                 RESULT 13
US-09-992-807-6
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RESULT 19
US-10-190-417-25
; Sequence 25. Application US/10190417
; Publication No. USZ0030166137A1
; GENERAL INFORMATION:
; APPLICANT: Caker, Charles S.
; APPLICANT: Chandrashekar, Jayaram
; APPLICANT: Chandrashekar, Jayaram
; APPLICANT: Hoon, Mark A.
; APPLICANT: The Regents of the United States of America
; APPLICANT: The Regents of the United States of America
; APPLICANT: The Regents of the United States of America
; APPLICANT: The Government of the United States of America
; APPLICANT: The Government of the United States of America
; APPLICANT: The Regents of the United States of America
; APPLICANT: The Government of the United States of America
; APPLICANT: The Government of the United States of America
; APPLICANT: The Government of the United States of America
; TILLE OF INVENTION: Mammalian Sweet and Amino Acid Heterodimeric Taste
; TILLE OF INVENTION WUMBER: US 60/302, 998
; PRIOR FILING DATE: 2001-003-03
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 25
; LENTH: SEB
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
FILE REFERENCE: 36-002810US/PC
CURRENT APPLICATION NUMBER: US/10/246,785
CURRENT FILING DATE: 2002-12-09
FRIOR APPLICATION NUMBER: US 60/323,450
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 858
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US-10-179-373-4
; Sequence 4, Application US/10179373
; Dublication No. US20030232407A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
                                                                                                                                                                                                                                 TYPE: PRT

ORGANISM: Rattus norvegicus
US-10-246-785-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rattus norvegicus
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US-10-190-417-25
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Best Local Similarity 83.3%
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GENERAL INFORMATION:
APPLICANT: Eyba, Nicholas J.P.
APPLICANT: Ryba, Nicholas J.P.
APPLICANT: Nelson, Greg
APPLICANT: Chandrashekar, Jayaram
APPLICANT: Chandrashekar, Jayaram
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the United States of America
APPLICANT: The Regents of the United States of America
APPLICANT: Department of Health and Human Services
TILLE OF INVENTION: Mammalian Sweet Taste Receptors
FILE REFERENCE: 02307E-120110US
CURRENT FILING DATE: 2001-08-10
FRIOR PILING DATE: 2001-08-10
FRIOR FILING DATE: 2001-07-03
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 25
LENGTH: 858
                                                                                                                                                                                                                                                                                                                               90.0%; Score 27; DB 11; Length 858; 83.3%; Pred. No. 9.8e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%; Score 27; DB 11; Length 858; 83.3%; Pred. No. 9.8e+02; live 1; Mismatches 0; Indels
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; OTHER INFORMATION: rat T1R3 sweet taste receptor
US-09-927-315-25
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US-10-246-785-9
Subjucted 9, Application US/10246785
Subjuction No. US2030148448A1
GENERAL INFORMATION:
APPLICANT: IRW, LLC
APPLICANT: The Scripps Research Institute
APPLICANT: The Scripps Research Institute
APPLICANT: Sheng, Ding
APPLICANT: Schultz, Peter G
TITLE OF INVENTION: Sweet Taste Receptors
            PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: 60/226,448

PRIOR FILING DATE: 2000-08-17

PRIOR APPLICATION NUMBER: 60/259,227

PRIOR PILING DATE: 2001-01-03

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.1

LENGTH: 858
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US-09-927-315-25
// Sequence 25, Application US/09927315
// Sublication No. US20030040045A1
// GENERAL INFORMATION
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-799-629-14
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86.7%; Score 26; DB 12; Length 18;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3<sup>3</sup>
....hes 5; Conservative
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ORGANISM: Homo sapiens
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SIDLEY 13
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          1 SVDVBY 6
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APPLICANT: 11, XIADONG
APPLICANT: T1, XIADONG
APPLICANT: COCONNELL, SHAWN
APPLICANT: O'CONNELL, SHAWN
APPLICANT: O'CONNELL, SHAWN
APPLICANT: O'CONNELL, SHAWN
APPLICANT: ADLER, JON
APPLICANT: XU, HONG
APPLICANT: XU, HONG
APPLICANT: XU, HONG
APPLICANT: XU, HONG
APPLICANT: NU, HONG
APPLICANT: SCHENGES, SAID RECEPTORS AND USE THEREOF FOR
ITILE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
ITILE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
APPLICATION NUMBER: US/10/179
PRIOR APPLICATION NUMBER: 60/304,749
PRIOR FILING DATE: 2001-06-26
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/310,493
PRIOR APPLICATION NUMBER: 60/310,493
PRIOR APPLICATION NUMBER: 60/312,090
PRIOR APPLICATION NUMBER: 60/314,143
PRIOR PILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/374,143
PRIOR PILING DATE: 2002-04-15
PRIOR PILING D
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US-10-035-045-14

| Sequence 14, Application US/10035045
| Publication No. US20030054448A1
| GENERAL INFORMATION:
| APPLICANT: ADLER, JON BLIOT
| APPLICANT: LI, XIAODONG
| APPLICANT: C) CONNELL, SHAWN
| APPLICANT: O'CONNELL, SHAWN
| APPLICANT: O'CONONELL, SHAWN
| PRIOR APPLICATION NUMBER: 60/259,27
| PRIOR APPLICATION NUMBER: 60/259,27
| PRIOR APPLICATION NUMBER: 60/284,547
| PRIOR PILING DATE: 2001-04-19
| NUMBER OF SEQ ID NOS: 24
| SEQ ID NO 14
| LENGTH: 858
| LENGTH: 858
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Best Local Similarity 83.3
Matches 5; Conservative
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RESULT 23
US-10-193-477-56
Sequence 56, Application US/10193477
Publication No. US20030195163A1
GENERAL INFORMATION:
TITLE OF INVENTION: DELICINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4, TITLE OF INVENTION: THEREOF
FILE REPERENCE: 10153 NP
CURRENT APPLICATION NUMBER: US/10/193,477
CURRENT FILING DATE: 2002-07-11
PRIOR FILING DATE: 2001-07-11
PRIOR PILING DATE: 2001-07-11
PRIOR PILING DATE: 2001-07-11
SPIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patentin version 3.1
SEQ ID NO 56
LENGTH: 18
US-10-369-493-1385

i) Sequence 1285, Application US/10369493

j) Sequence 1285, Application US/10369493

j) Publication No. US20030233675A1

j) GENERAL INFORMATION:
    APPLICANT: Hinkle, Green V.
    APPLICANT: Slater, Steven C.
    APPLICANT: Goldman, Barry S.
    APPLICANT: USANTION: PLANTS WITH IMPROVED PROPERTIES
    FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    FILE REFERENCE: 38-10(52052)B
    CURRENT FILING DATE: 2003-02-28
    PRIOR APPLICATION NUMBER: US 60/360,039
    PRIOR APPLICATION NUMBER: US 60/360,039
    PRIOR APPLICATION NUMBER: US 60/360,039
    NUMBER OF SEQ ID NOS: 47374
    SEQ ID NO 1385
    LENGTH: 1471
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Gaps
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APPLICANT: Outun, Kerry B.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Spytek, Kimbara, Padigaru
APPLICANT: Spytek, Kimbaray A.
ITILE OF INVENTION: POlypeptides and Nucleic Acids Encoding Same
PILES REFERENCE: 15966-620 CIP
CURRENT APPLICATION NUMBER: US/09/137,149
CURRENT APPLICATION NUMBER: 60/170,564
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,562
PRIOR PLING DATE: 1999-12-27
PRIOR PAPLICATION NUMBER: 60/173,549
PRIOR PLING DATE: 2000-01-04
PRIOR PLING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR PLING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB 9;
Pred. No. 5e+02;
2; Mismatches
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 60/174,962
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/223,929
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 49
; SOFTMARE: PATENTIN Ver. 2.0
; SEQ ID NO 42
; LENGTH: 284
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; Publication No. US2033233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 12, Application US/09737149; Patent No. US20020077466A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.7%;
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Rattus norvegicus
US-09-737-149-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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US-09-737-149-12
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Best Local Similarity
Matches 4; Conserv
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2 AVDIEY 7
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                                                                                                                                                                                APPLICANT: Spaderna, steven A
APPLICANT: Spaderna, steven A
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE REFERENCE: 1596-620 CIP
CURRENT APPLICATION NUMBER: US/09/737,149
CURRENT APPLICATION NUMBER: 60/170,564
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR PILING DATE: 1999-12-27
PRIOR PILING DATE: 1999-12-27
PRIOR PILING DATE: 1999-12-27
PRIOR PILING DATE: 1999-12-27
PRIOR FILING DATE: 2000-01-07
PRIOR PILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
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APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Shinkers, Richard A.
APPLICANT: Shinkers, Richard A.
APPLICANT: Muralidara. Padigaru
APPLICANT: Muralidara. Padigaru
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-620 CIP
CURRENT FILING DATE: 1099-12-14
PRIOR PILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR PILING DATE: 1999-12-29
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LOCATION: (1)...(282)

LOCATION: (1)...(282)

OTHER INFORMATION: Where X is a residue at which the query and confer INFORMATION: subject seugnces are not identical.

US-09-737-149-43
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66.7%; Pred. No. 5e+02;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Consensus Seguence
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Patent No. US20020077466A1
GENERAL INFORMATION:
    US-09-737-149-43
Sequence 43, Application US/09737149
Patent No. US20020017466A1
GENERAL INFORMATION:
APPLICANT: Spaderna, Steven K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Best Local Similarity 66.7
Matches 4; Conservative
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2 AVDIEY 7
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RESULT 31
US-10-289-762-1049
US-10-289-762-1049
Sequence 1049, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
TITLE REPERENCE: 9710-003-999, 762
TITLE REPERENCE: 9710-003-999, 762
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-7
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1049
LENGTH: 358
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0
                                                                                                                                                                                                                                                                       Length 322;
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                                                                                                                                                                                                                                                                          86.7%; Score 26; DB 12; I 100.0%; Pred. No. 5.7e+02;
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Pred. No. 6.2e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20030119018A1
| Publication No. US20030119018A1
| GENERAL INFORMATION:
| APPLICANT: OMURA, SATOSHI
| APPLICANT: ISHIKAWA, JUN
| APPLICANT: ISHIKAWA, JUN
| APPLICANT: SHIBA, TADAYOSHI
| APPLICANT: SHIBA, TADAYOSHI
| APPLICANT: SHIBA, TADAYOSHI
| APPLICANT: HATTOR! WASAHIRA
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
| FILE REFERENCE: 249-262
| CURRENT APPLICATION NUMBER: US/10/156,761
| CURRENT PILING DATE: 2001-05-39
| PRIOR FILING DATE: 2001-05-39
| PRIOR FILING DATE: 2001-06-05
| NUMBER: BEQ 1001-05-30
| PRIOR FILING DATE: 2001-06-05
| NUMBER: APPLICATION NUMBER: JESON-05-39
| PRIOR FILING DATE: 2001-06-30
| ERNGTH: 349
                                                                                                                                                                                                                                                                                                                          0; Mismatches
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19942
LENGTH: 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12808
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ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                        TYPE: PRT
CRGANISM: Anabaena PCC7120
US-10-369-493-19042
                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 5; Conservative
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US-10-156-761-12808
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goidman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROFERTIES
FILE REPERENCE: 38-10(5.005.2)8
CURRENT PELLING NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PELLING DATE: 2002-02-1
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22955
LENGTH: 305
     APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16538
LENGTH: 287
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APPLICANT: Gac, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: THE PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                             86.7%; Score 26; DB 12; Length 287; 100.0%; Pred. No. 5.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22855, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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US-10-369-493-19042
// Sequence 19042, Application US/10369493
// Publication No. US20030233675A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-369-493-16538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Aeropyrum pernix
US-10-369-493-22955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 VDVEY 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VDVEY 6
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US-10-369-493-22955
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RESULT 35
US-10-369-493-2914
Sequence 2914, Application US/10369493
Sequence 2914, Application US/10369493
Publication No. US2003023367541
Septence 2014, Application US/2003023367541
SPENDICANT: Cao, Yongwei
APPLICANT: Garer's Keeven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITILE OF INVENTION: DAMES 2003-02-28
PRIOR APPLICATION UNMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NOS: 47374
SEQ ID NOS: 47374
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Similarity 66.7%; Pred. No. 9.1e+02;
4; Conservative 2; Mismatches 0; Indels
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Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                            Sequence 5999, Application US/09738626
; Publication No. US2020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: TATEISHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TYERISHI, NACKO
APPLICANT: TYERISHI, NACKO
APPLICANT: TYERISHI, NACKO
APPLICANT: SENOH, AKIHRO
APPLICANT: SENOH, AKIHRO
APPLICANT: SENOH, AKIHRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US 99/337484
PRIOR FILING DATE: 2000-04-07
PRIOR PELICATION NUMBER: JP 90/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PRECENTIN VET: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 TVDIEY 271
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Best Local Similarity
Matches 4; Conserv
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54 VDVBY 58
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bublication No. US20030233675A1

publication No. US20030233675A1

general invormation.

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

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; Bublication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: Cao, Yongwei
    APPLICANT: Slater, Steven C.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Chen, Xianfeng
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
    TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION NUMBER: US 60/360,039
    PRIOR PRILING DATE: 2002-02-21
    NUMBER OF SEQ ID NOS: 47374
    SEQ ID NO 12245
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                                                                       86.7%; Score 26; DB 12; Length 358; 100.0%; Pred. No. 6.4e+02; rive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 395;
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Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Methanobacterium thermoautotrophicum
US-10-369-493-1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT CRGANISM: Aspergillus nidulans US-10-369-493-13245
                                                Query Match
Best Local Similarity luv.
S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
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148 VDVEY 152
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US-10-369-493-13245
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US-10-369-493-1147
               US-10-289-762-1049
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Sequence 21, Application US/10093037
Sequence 21, Application US/10093037
Sequence 21, Application US/20030078397A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Machini, Edward
APPLICANT:
APP
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APPLICATION WIMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 08010/024002
TELECOMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 anino acids
TYRE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 26; DB 14; I
100.0%; Pred. No. 9.4e+02;
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PRIOR FILING DATE: 2001-07-20
PRIOR PILING DATE: 1090-08-13
PRIOR PILING DATE: 1996-08-13
PRIOR PILING DATE: 1997-10-10
PRIOR PLING DATE: 1997-10-10
PRIOR PILING DATE: 1997-10-10
PRIOR PILING DATE: 1997-10-06
NUMBER OF SEQ ID NOS: 72
SOFTWARE: F8SESEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Thermococcus chitonophagus US-10-093-037-21
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Publication No. US20030232378A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 VDVEY 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VDVEY 6
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                                                                                                                                                                                                                                                          Sequence 11, Application US/10193896

Sequence 11, Application US/10193896

Pub.idence 10 NO US20030129710A1

SEQUENCE 11 FORMATION

SEQUENCE 1 FOR SET INSTITUT

SPELICANT: Blotcknologisk Institut

APPLICANT: Blotcknologisk Institut

APPLICANT: Stougaard, Feter

APPLICANT: Brithalen, Hans

APPLICANT: Brithalen, Karen

APPLICANT: Brithalen, Karen

APPLICANT: Brithalen, Karen

APPLICANT: Brithalen, Hans

APPLICANT: Brithalen, Hans

APPLICANT: Brithalen, Hans

APPLICANT: Brithalen, Hans

APPLICANT: Brithalen, Karen

APPLICANT: Brithalen, Hans

APPLICANT: Bottcher, Karen

APPLICANT: Bott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%; Score 26; DB 16; Length 496; 66.7%; Pred. No. 9.1e+02; ive 2; Mismatches 0; Indels
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Publication No. US2002015555041

GENERAL INFORMATION:

TITLE OF INVENTION: GLYCOSIDASE ENZYMES

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSE: Gray Cary Ware & Freidenrich LLP

STREET: 4365 Executive Drive, Suite 1600

CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Diskette
COMPUTER: IBM Compatible
OPREATING SYSTEM: Windowes
OPERATING SYSTEM: Windowes
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/121,032
FILING DATE: 09-Apr-2002
CLASSIFICATION OFTA: VINKNOWN->
PRIOR APPLICATION UNDRER: US/09/134,078
APPLICATION NUMBER: US/09/134,078
APPLICATION NUMBER: 08/949,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
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451 AIDVEY 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: T.maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conserv
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US-10-121-032-21
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APPLICANT: ELLEKANAN ARKEN
APPLICANT: ELLEKANAN ARKEN
APPLICANT: ELLEKANAN ARKEN
APPLICANT: ERSTELLI, LUCA
APPLICANT: ERSTELLI, LUCA
APPLICANT: ERSTELLI, LUCA
APPLICANT: ERSTELLI, LUCA
APPLICANT: SERVENCEN, SERVAN
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
CURRENT FILING DATE: 2001-09-18
RIOR FILING DATE: 2001-09-18
RIOR FILING DATE: 2001-01-013
RIOR PELLOR PAPLICATION NUMBER: 60/260, 913
RIOR PELLOR DATE: 2001-01-013
RIOR PELLOR DATE: 2001-01-013
RIOR APPLICATION NUMBER: 60/260, 913
RIOR PELLOR DATE: 2001-01-013
RIOR PELLOR DATE: 2001-01-013
RIOR APPLICATION NUMBER: 60/23, 96
RRIOR FILING DATE: 2001-01-03-09
RRIOR PELLOR DATE: 2000-09-15
RRIOR RELING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Unknown Organism: NOVX Polypeptide
                                                                                                               Sequence 18, Application US/09954342
Publication No. US20030170838A1
GENERAL INFORMATION:
APPLICANT: SPYTEK, KIMBERLY ANN
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: USRNET, CORNEN, STEVEN D.
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: COLMAN, SIEVEN D.
APPLICANT: COLMAN, LINDA
APPLICANT: TCHERNEV, VELIZAR T.
APPLICANT: TCHERNEV, VELIZAR T.
APPLICANT: SHENOY, SURESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PADIGARU, MURALIDHARA
GERLACH, VALERIE L.
MACDOUGALL, JOHN R.
SMITHSON, GLENNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMITHSON, GLENNDA
MILLET, ISABELLE
PEYMAN, JOHN
STONE, DAVID
GUNTHER, ERIK
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLLERMAN, KAREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-954-342-18
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Pred. No. 1e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DASSELDEAN, NOWELL
APPLICANT: Oblight, Nation
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Traminco, Robert T.
APPLICANT: Carr, Grant J.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENT FILING DATE: 2000-03-21
CURRENT PRING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/25,727
PRIOR PELING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 13170
TENNATH: 572
HILL OF INVENTION: MOVEL TOLL MOLECULES AND USES THEREOF
FILE REFERENCE: MNI-08
CURRENT APPLICATION NUMBER: US/10/461,747
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/09/586,340
PRIOR APPLICATION NUMBER: 06/137,659
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 548
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Pred. No. 1.1e+03;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13170, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Streptococcus pneumoniae US-09-815-242-13170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-10-461-747-2
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518 SIDLEY 523
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Best Local Similarity
Matches 4; Conserv
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ORGANISM:
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DB 12;

86.7%; Score 26;

Query Match

204 AVDIĖY 209

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Gaps

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APPLICANT: WIGHTA, VISHUU S.
APPLICANT: WIGHTA, VISHUU S.
APPLICANT: TAUPIER X. RAYMOND J.
APPLICANT: TAUPIER X. RAYMOND J.
APPLICANT: TAUPIER X. RAYMOND J.
APPLICANT: COLANA; TEVEN D.
APPLICANT: COLANA; TEVEN D.
APPLICANT: TEVEN D.
APPLICANT: TEVEN Y. RAILER T.
APPLICANT: TEVEN Y. RAILER T.
APPLICANT: TEVEN Y. RAILER T.
APPLICANT: GREAGA, VALERIE M.
APPLICANT: GREAGA, VALERIE M.
APPLICANT: GREAGA, VALERIE M.
APPLICANT: STONE, DAVID
APPLICANT: GREAGA, CALENDA
APPLICANT: STONE, DAVID
APPLICANT: GREAGE, GAVID
APPLICANT: GROWEN, DAVID
APPLICANT: GROWEN, DAVID
APPLICANT: GROWEN, GARRIN
APPLICANT GROWEN, GARRIN
APP
; ORGANISM: Unknown Organism
FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: NOVX Polypeptide
US-09-954-342-20
                                                                                                                                                                                                                               .
0
                                                                                                                                                            Length 606;
                                                                                                                                                                                                                           0; Indels
                                                                                                                                                     Query Match
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 43
US-09-954-342-42
US-09-954-342-42

, Sequence 42, Application US/09954342

; Publication No. US20030170838A1

; GENERAL INFORMATION:
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576 SIDLEY 581
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FILE OF INVENTION: NOVEL POLYNUCLECTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE APPLICATION NOVEL POLYNUCLECTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 1202-14
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/240,498
PRIOR APPLICATION NUMBER: 60/260,284
PRIOR PLING DATE: 2001-01-09
PRIOR PLING DATE: 2001-01-09
PRIOR PLING DATE: 2001-01-01
PRIOR PLING DATE: 2001-01-19
PRIOR PLING DATE: 2001-01-11
PRIOR PLING DATE: 2001-01-11
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-13
PRIOR PLING DATE: 2001-01-13
PRIOR PLING DATE: 2001-01-13
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-15
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0
      Best Local Similarity 66.7%; Pred. No. 1.1e+03; Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MISHRA, VISHNU S.
APPLICANT: SPYTEK, KIMBELLY ANN
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: COLMAN, LINDA
APPLICANT: TCHERNEY, VELIZAR T.
APPLICANT: SHENOY, SURESH
APPLICANT: GERLACH, WIRALIDHARA
APPLICANT: GERLACH, VALERIE L.
APPLICANT: SHENOY, SURESH
APPLICANT: SMITHSON, GLENNDA
APPLICANT: SMITHSON, GLENNDA
APPLICANT: STONE, DAVID
APPLICANT: STONE, DAVID
APPLICANT: STONE, DAVID
APPLICANT: ELLERWAN, KAREN
APPLICANT: GUNTHER, ERIK
APPLICANT: GUNTHER, ERIK
                                                                                                                                                                                                                                                                RESULT 42
US-09-954-342-20
'Sequence 20, Application US/09954342
', Publication No. US20030170838A1
', GENERAL INFORMATION:
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RASTELLI, LUCA
ZERHUSEN, BRYAN
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576 SIDLEY 581
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APPLICANT: James applicant: James applicant: James applicant: James applicant: Tiehkoff, Daniel applicant: Tiehkoff, Daniel applicant: Tiehkoff, Daniel applicant: Zerobkin, Alexey M applicant: Eroshkin, Alexey M applicant: Construction: Methods of Use TITLE OF INVENTION: Methods of Use FILE OF INVENTION: Methods of Use FILE OF INVENTION: MURBER: US 5002-04-23 CURRENT APPLICATION NUMBER: US 60/285,697 PRIOR APPLICATION NUMBER: US 60/285,697 PRIOR FILING DATE: 2001-04-27 PRIOR PLING DATE: 2001-06-05 PRIOR PLING DATE: 2001-06-05 PRIOR FILING DATE: 2001-07-09 PRIOR FILING DATE: 2001-07-09 PRIOR FILING DATE: 2001-07-09 PRIOR FILING DATE: 2001-07-09 PRIOR PRIOR FILING DATE: 2001-08-31 NUMBER OF SEQ ID NOS: 8603 SOFTWARE: Patentin version 3.1 SEQ ID NO 3395 LENGTH: 694 TWOND THE CONTRACT SECONT S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT PELINGE: 084335/0160
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR PILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PALENTIN VET: 2:1
SOFTWARE: PALENTIN VET: 2:1
LENGTH: 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3395, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 47
18-10-128-1395
; Sequence 8395, Application US/10128714
; Publication No. US20030119013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3395
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Best Local Similarity 66.7-
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-094-749-2513
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576 SIDLEY 581
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US-10-128-714-3395
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Sequence 4, Application US/10193477

Sequence 4, Application US/10193477

PUDIcation No. US2003019516341

GENERAL INFORMATION:

TITLE OF INVENTION: ELICIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS

TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,

TITLE OF INVENTION: THEREOF

FILE REFERENCE: D0153 NP

CURRENT APPLICATION NUMBER: US/10/193,477

CURRENT PLING DATE: 2002-07-11

PRIOR PLING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US 60/372,147

PRIOR APPLICATION NUMBER: US 60/372,147

NUMBER OF SEQ ID NOS: 229

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 606

THENTH: 606
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                                                                                                                                                                                                                                                                                 86.7%; Score 26; DB 12; Length 606; 66.7%; Pred. No. 1.1e+03; Live 2; Mismatches 0; Indels
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US-10-094-749-2513
Sequence 2513, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: SOGAI, TAKAO
APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: STORICANT SPECIAL
APPLICANT: STO, HIROWIKI
APPLICANT: SHI, SHIZUKO
APPLICANT: ISHI, SHIZUKO
APPLICANT: ISHI, SHIZUKO
APPLICANT: ISHIO, YUUKO
APPLICANT: ISHIO, YUKI
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SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
               PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7°
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Best Local Similarity bo...
4, Conservative
                                                                                                   SEQ ID NO 42
LENGTH: 606
TYPE: PRT
CRGANISM: Homo sapiens
US-09-954-342-42
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ORGANISM: Homo sapiens
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576 SIDLEY 581
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APPLICANT: Cao, Yongwei
APPLICANT: Hintle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 281, Application US/10291265
; Bequence 281, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al.
; TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides
; TILE REFERENCE: 21272-017 (785)
; CURRENT FAPLICATION NUMBER: 09/491,404
; FILE REFERENCE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR PELING DATE: 2000-01-25
; PRIOR PELING DATE: 2000-09-15
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SEQ ID NO 281
; LENGTH: 968
; TENDER PRIOR PRIOR WINDER: 09/631,451
; LENGTH: 968
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                                                                                                  RESULT 49
US-10-369-493-22944
VS-10-369-494, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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; ORGANISM: Aeropyrum pernix
US-10-369-493-22944
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Best Local Similarity 83.3
Matches 5; Conservative
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; ORGANISM: Homo sapiens
US-10-291-265-281
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283 SVEVEY 288
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            214 VDVEY 218
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GENERAL INFORMATION:

APPLICANT: Jiang, Bo.

APPLICANT: Hu, Wenqi

APPLICANT: Hu, Wenqi

APPLICANT: Hu, Wenqi

APPLICANT: Zamudio, Carlos

APPLICANT: Zamudio, Carlos

APPLICANT: Zamudio, Carlos

APPLICANT: Lemieux, Sebastien M

TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

TITLE OF INVENTION: Methods of Use

FILE REFERENCE: 10182-018-99

CURRENT APPLICATION NUMBER: US 60/285,697

PRIOR FILING DATE: 2001-04-23

PRIOR FILING DATE: 2001-04-27

PRIOR FILING DATE: 2001-04-27

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-31

PRIOR FILING DATE: 2001-06-31

NUMBER OF SEQ ID NOS: 8603

SOFTWARE: PatentIn version 3.1

FEAGLE OF SEG ID NOS: 8603

FEAGLE OF SEG ID NOS: 8603
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86.7%; Score 26; DB 12; Length 725;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels
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) LOCATION: (1)..(725)

) OTHER INFORMATION: unsure at all Xaa locations

US-10.-369-493-4017
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-8395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Search completed: January 20, 2004, 14:02:42

Job time : 33 secs

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Sequence 18, Appl Sequence 34, Appl Sequence 3, Appl Sequence 4, Appl Sequence 4507, Ap Sequence 5104, Ap Sequence 32787, A Sequence 32787, A Sequence 32787, A Sequence 3, Appl Sequence 4, Appl Sequence 521, Appl Sequence 521, Appl Sequence 521, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 23, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 39, Appl Sequence 491, Appl Sequence 491, Appl Sequence 491, Appl Sequence 2, Appl Sequence 6, Appl Market 6, Appl Market
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US-08-17

Sequence 1, Application US/08759599

Sequence 1, Application US/08759599

Patent No. 59170N:

APPLICANT: Rabkin, Simon

APPLICANT: Rystal, Gerald

ITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO

TITLE OF INVENTION: AMELIORATE CELL DEATH

NUMBER OF SEQUENCES: 12

CORRESPONDENCES: 12

CORRESPONDENCE SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington
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             US-07-854-5968-47
US-07-854-5968-47
US-07-854-5968-49
US-07-854-5968-40
US-07-854-5968-40
US-09-211-542A-4
US-08-488-940-4
US-08-488-940-1
US-08-128-352-7836
US-09-328-352-7836
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US-09-328-352-7836
US-09-328-352-7836
US-09-252-991A-20153
US-09-252-991A-17980
US-09-252-991A-17980
US-09-252-991A-17980
US-09-252-991A-17980
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US-09-252-991A-17980
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US-09-134-0010-5021
US-09-134-05-5021
US-09-134-076-21
US-09-134-078-2
US-09-270-917-2
US-08-989-299-11
US-09-134-0010-4931
US-09-134-0010-4931
US-09-134-0010-5322
US-09-134-110-2
US-09-134-1110-2
US-09-134-1110-2
US-09-134-1110-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
Sequence 5, Applisequence 6, Applisequence 6, Applisequence 7, Applisequence 17, Applisequence 12, Applisequence 31, Applisequence 31, Applisequence 3, Applisequence 1, Applisequence 1, Applisequence 1, Applisequence 2, Applise
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(without alignments)
11.539 Million cell updates/sec
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1: /cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                           328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 75 summaries
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Perfect score:
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                                                                                                                                   Run on:
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No.
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HILLS OF INVENTION: No. 6348567el Peptides and Their Use to TITLE OF INVENTION: No. 6348567el Peptides and Their Use to TITLE OF INVENTION: Ameliorate Cell Death FILE REPRENCE: 50246703003 CURRENT APPLICATION NUMBER: US/09/294,457 CURRENT PRING DATE: 1999-04-19 PRIOR APPLICATION NUMBER: US 08/759,599 PRIOR FILING DATE: 1996-12-05 PRIOR PELING DATE: 1996-12-06 NUMBER OF SEQ ID NOS: 16 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: DATE: 1995-12-06 NUMBER OF SEQ ID NOS: 16 NUMBER OF SEQ ID N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 4; Length 16; 100.0%; Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Krystal, Gerald
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELICANTE CELL DEATH
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER RELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,599
FILING DATE: OS-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEMASTERS, DAVID D.
REGISTRATION NUMBER: 33.963
REPRENCE/DOCKET NUMBER: 78059.401
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEX: 37.3836
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TENCH. 18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Synthetic polypeptide US-09-294-457-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08759599
Patent No. 5917013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 6; Conservative
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MOLECULE TYPE: pept
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Patent No. 6348567

GENERAL INFORMATION:

APPLICANT: Krystal, Gerald

APPLICANT: Rabkin, Simon W.

TITLE OF INVENTION: Amelicrate Cell Death

FILE REFERENCE: 50216/003003

CURRENT FILING DATE: 1999-04-19

FRIOR PELING DATE: 1999-04-19

PRIOR FILING DATE: 1995-12-05

PRIOR FILING DATE: 1995-12-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 6

LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 30; DB 2; Length 6; Best Local Similarity 100.0%; Pred. No. 2.5e+05; Matches 6; Conservative 0; Mismatches 0; Indels
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                                     CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/759,599

FILING DATE: 05-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MCMAStels, David D.

REGISTATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 780059.401

TELEPAATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 780059.401

TELEPAATION INFORMATION:

TELEPAATION INFORMATION:

TELEPAACH SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENDTH: 6 amino acids
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; OTHER INFORMATION: Synthetic polypeptide
US-09-294-457-1
                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-294-457-5
Sequence 5, Application US/09294457
Patent No. 6348867
GENERAL INPORMATION:
APPLICANT: Krystal, Gerald
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / MOLECULE TYPE: peptide
US-08-759-599-1
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Best Local Similarity
Matches 6; Conserv
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US-09-294-457-1
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Gaps

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Query Match
Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-759-599-6
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                                                                                                                                               Sequence 6, Application US/09294457
Patent No. 6348567
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Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,599
FILING DATE: 05-DEC-1995
CLASSIFICATION: 435
               APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
APPLICAT: Rabkin, Simon W.
TITLE OF INVENTION: No. 6348867el Peptides
TITLE OF INVENTION: Ameliorate Cell Death
FILE REFERENCE: 50216/003003
CURRENT APPLICATION NUMBER: US/09/294,457
CURRENT FILING DATE: 1999-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
PRIOR APPLICATION NUMBER: US 08/759,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 780059.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rabkin, Simon
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE
TITLE OF INVENTION: AMELIORATE CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (200, TELEFAX: 3723836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (200) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McMasters, David D.
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linear
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; Mismatches
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                                                                                and
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                                                                                  Their Use
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                                            1 SYDVEY 6
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; MOLECULE TYPE: peptide US-08-759-599-7
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Query Match
Best Local S
Matches 6
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Best Local S
Matches 6
                                                                                                                    TELEPAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/759,599
FILING DATE: 05-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Appl Patent No. 59170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rabkin, Simon
APPLICANT: Krystal, Gerald
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PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                    NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 780059.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO TITLE OF INVENTION: AMELIORATE CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washing
                                                                                                             TOPOLOGY:
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Similarity 100.0%;
6; Conservative 0
 Similarity 6; Conserv
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                                                                                                                                                                                                                                       (206) 682-6031
   Conservative
                                                                                                         ss: single
linear
                100.0%; Score 30; DB 2; Length 21; 100.0%; Pred. No. 1.4;
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                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION: 1653
PRIOR APPLICATION: 1653
PRIOR APPLICATION NUMBER: 60/069,497
APPLICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
APPLICATION TIPORMATION:
APPLICATION TIPORMATION:
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Applic Patent No. 6348567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Reed,
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CURRENT APPLICATION NUMBER: US/09/294,457
CURRENT FILING DATE: 1999-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: No. 6348567el Peptides and Their Use
TITLE OF INVENTION: Ameliorate Cell Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Krystal, Gerald APPLICANT: Rabkin, Simon
TELEFAX: (617)443-0004
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 7
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                NAME: Attorney, Strimpel, Harriet M. REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                (617)443-9292
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Pred. No.
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RESULT 11 US-07-854-596B-31

GENERAL INFORMATION:

APPLICANT:

Dawson, Keith M Hunter, Michael G Czaplewski, Lloyd tent No.

1, Application US/07854596B 5434073

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US-09-211-542A-12
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                                                                                                                                     Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
UNMEY ABSENCE OF THE OR 
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                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)443-0004
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Attorney, Strimpel, Harriet M.
REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
                                                                                                                                                                      Local Similarity
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99 SVDVEY 104
                                                                 1 SVDVEY 6
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                      Score 30; DE
Pred. No. 31;
                                                                                                                                     Mismatches
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Proteins and nucleic acids

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                                                                   ; LENGTH: 372
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-374-038-3
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US-09-374-038-3
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     Matches
                               Query Match
                                                                                                                                 SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                                                 Patent No. 6309873
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6309873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/374,038
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                    APPLICANT:
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
ITTLE OF INVENTION: STREPTOKINASE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line
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LENGTH: 369 amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILLING DATE: 03-UN-1992
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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 Similarity 6; Conserv
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                                                                                                                                                    PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09374038
                                                                                                                                                                                                                                                                                                                                                 Madrazo, Isis Del Carmen
Garcia, Jose De Jesus De
                                                                                                                                                                                                                                                                                                                                    Ojalvo, Ariana Garcia
                                                                                                                                                                                                                                                                                                Menendez, Alina Seralena
Escalona, Elder Pupo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; ilarity 100.0%; Conservative 0
100.0%; Score 30; DB ilarity 100.0%; Pred. No. 33; Conservative 0; Mismatches
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La Fuente
                                DB 4; Length 372;
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APPLICANT: Menendez, Alina Garcia
APPLICANT: Escalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Gitego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Wetches 6; Conserve
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APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14
Patent No. 6413759
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                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/374,038
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09658179 Patent No. 6413759
                                                                   Matches
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APPLICANT:
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CURRENT FILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                          TYPE: PRT ORGANISM: Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                               Local Similarity
les 6; Conserv
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157 SYDVEY 162
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157 SVDVEY 162
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                                1 SYDVEY 6
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Garcia, Jose De Jesus De
Ojalvo, Ariana Garcia
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Garcia, Jose De Jesus De
Ojalvo, Ariana Garcia
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Escalona, Elder Pupo
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                                                                 Conservative
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                                                               100.0%; Score 30; DB
100.0%; Pred. No. 34;
tive 0; Mismatches
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                                                                                                DB 4; Length 384;
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SVDVEY 6

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RESULT 17
US-09-658-179-1
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LENGTH: 401
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Matches
                                     Sequence 1, Application US/09658179 Patent No. 6413759
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Patent No. 6309873
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Best Local Similarity
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LENGTH: 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/374,038
CURRENT FILING DATE: 199-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver: 2.1
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APPLICANT: Escalona, Elder Bretandez
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
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APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Ojalvo, Ariana Garcia
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CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREEFFOKINASE MUTANTS
FILE REFERENCE: Sequence Listings 1-14 re: 976-5
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APPLICANT: Garcia, Jose De Jesus De La Fuente
APPLICANT: Ojalvo, Ariana Garcia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Streptococcus equisimilis
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                 INFORMATION:
                                                                                                                                                                 144 SVDVEY 149
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Escalona, Elder Pupo
                                                                                                                                                                                                                                                  Conservative
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Isis Del Carmen Torrens
                                                                                                                                                                                                                                               100.0%; Score 30; DB
100.0%; Pred. No. 36;
tive 0; Mismatches
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APPLICANT: Garce,
APPLICANT: Ojalvo, Ariana Garce,
APPLICANT: Menendez, Alina Seralena
APPLICANT: Mesendez, Alina Seralena
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
TITLE OF INVENTION: STREPTOKINASE MUTANTS
TOTE PREPERENCE: Sequence Listings 1-14 re: 976-5
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US-08-759-599-12
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; TYPE: PRT
; ORGANIEM: Streptococcus equisimilis
US-09-658-179-1
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Query Match
Best Local Similarity
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Best Local Similarity 100.0%; Pred. No.
Matches 6; Conservative 0; Mismatch
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APPLICANT: Rabkin, Simon
APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE
TITLE OF INVENTION: AMELIORATE CELL DEATH
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/658,179
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                    TELEFAX: (206) 682-603
TELEX: 3723836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 780059.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEFX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                 NAME: McMasters, David REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/759,599 FILING DATE: 05-DEC-1995 CLASSIFICATION: 435
                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                          TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
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    100.0%;
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    Score 30;
Pred. No.
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    DB 2;
37;
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                       Length 413;
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Query Match
Best Local Similarity
Matches 6; Conserve
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US-09-294-457-12
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; ORGANISM: Streptococcus equisimilis
US-09-374-038-2
                                                                                                                                      US-09-294-457-12
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US-09-374-038-2
                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12
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SEQ ID NO 2
                                                           Matches
                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: No. 6348567el Peptides and Their Use to
TITLE OF INVENTION: Ameliorate Cell Death
FILE REFERENCE: 50216/003003
CURRENT APPLICATION NUMBER: US/09/294,457
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: US 08/759,599
PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR PILING DATE: 1995-12-06
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APPLICANT:
APPLICANT:
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APPLICANT:
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CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
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APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                      OTHER INFORMATION: Synthetic polypeptide
                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                             TYPE: PRT
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   1 SVDVEY 6
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                                                           6; Conservative
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Garcia, Jose De Jesus De La Fuente
Ojalvo, Ariana Garcia
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Escalona, Elder Pupo
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                                                           100.0%; Score 30; DB 4; Length 413; 100.0%; Pred. No. 37; ive 0; Mismatches 0; Indels
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; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-179-2
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SEQ ID NO 2
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CURRENT APPLICATION NUMBER: US/09/658,179
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 14
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Madrazo, Isis Del Carmen Torrens
APPLICANT: Garcia, Jose De Jesus De La Fuent
APPLICANT: Ojalvo, Ariana Garcia
APPLICANT: Menendez, Alina Seralena
APPLICANT: Escalona, Elder Pupo
APPLICANT: Masso, Julio Raul Fernandez
APPLICANT: Griego, Martha De Jesus Gonzalez
TITLE OF INVENTION: STREPTOKINASE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
TELEFAX: (617)443-0004
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                       NAME: Attorney, Strimpel, Harriet M. REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     APPLICATION NUMBER: US/09/211,542A
FILING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,497
                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                    FILING DATE: 15-December-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: BANUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 125 S
CITY: Boston
STATE: Massac
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                                                         TELEPHONE:
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Garcia, Jose De Jesus De La Fuente
Ojalvo, Ariana Garcia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 Summer Street
                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BROMBERG & SUNSTEIN, LLP
                                                         (617)443-9292
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                   <u>ه</u>.
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RESULT 23
5240845-1
;Patent No. 5240845
;APPLICANT: FUJI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FUJII, SETSURO;TAKADA, KAORUKO;. KATANO, TAMIKI MAJIMA, EIJI;OGINO, KOICHI;ONO, KENJI;SAKATA, YASUYO;UENOYAMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/7/854,596B
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDONNell, John J
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MUTATED STREPTOKINASE PROTEINS NUMBER OF SECURICES: 65 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/549,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
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hes 6; Conservative
                                                                                                                                                                                                                                                                         STREET: Year CTTY: Chicago
                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION: Proteins and nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 414
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OGY: linear
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                  92,337
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Pred. No. 37;
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Pred. No. 37;
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US-07-854-596B-1-9
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                                                                                                                             ; MOLECULE TYPE: protein US-07-854-596B-19
                                                            Query Match
Best Local S
Matches 6
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 415 amino acid
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acid
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATECATION DATA:
APPLICATION NUMBER: US/07/854,596B
                                                                                                                                                                                                                                                                     NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 10.
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                                                                                                                                                                                                                              TELEFAX: 510-221
                                                                                                                                                          LENGTH: 435 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
178 SVDVEY 183
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                               1 SVDVEY 6
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                                                            Similarity 6; Conserv
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                                                            Conservative
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                                                           100.0%; Score 30; DI
100.0%; Pred. No. 39,
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                   92,337
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                                                                                          DB 1; Length 435;
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RESULT 26 US-07-854-596B-15

Sequence 15, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

PPLICANT: Dawson, Keith M PPLICANT: Hunter, Michael G PPLICANT: Czaglewski, Lloyd G ITLE OF INVENTION: Proteins and nucleic acids

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RESULT 27
US-08-560-098A-52
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acid
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                            TITLE OF INVENTION: Proteins having Fibrinolytic and TITLE OF INVENTION: Coagulation-inhibiting Properties NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/854,596B FILING DATE: 03-JUN-1992 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                          CITY: Washington
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les 6; Conserv
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Pred. No. 40;
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Suite 700
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100.0%;

Best Local Similarity 100.0%;

Matches 6; Conservation
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Patent No. 5434073
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Best Local &
                                                                                                                                                                       TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,3
TELECOMMUNICATION INFORMATION:
TELECHIONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: P 44 40 E
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPh D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Relear
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O:
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Czaplewski, Lloyd
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                   TELEFAX: 312-715-1234
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                                                                                                                                                           LENGTH:
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                                                                                                                                                             483 amino acids
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                                                                                                       protein
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                               Score 30; DB
Pred. No. 44;
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                                                DB 1; Length 483;
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Mismatches

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226 SVDVEY 231

SVDVEY

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RESULT 30
US-07-854-596B-28
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US-07-854-596B-47
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
                                                                                                                                                                                                                             Sequence 28, Application US/07854596B Patent No. 5434073
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47, Application US/07854596B Patent No. 5434073
                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-UN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Proteins and nucleic acids NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd
                                                                                                                       TITLE OF INVENTION: Proteins and nucleic acids NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Chicago
                                                                                                      ORRESPONDENCE ADDRESS:
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Local Similarity 100.0%;
hes 6; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: IL COUNTRY: USA
                                                                                    ADDRESSEE:
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DUNTRY: U
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     ASĎ
                                                 Chicago
                                                                 E: Dr. John J. McDonnell
Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 amino acids
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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RESULT 31
US-09-211-542A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,54
FILING DATE: 15-December-1998
CLASSIFICATION: 1653
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,497
FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                TELEFAX: (617)443-000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SEQUENCE CHARACTERISTICS:
LENGTH: 736 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: BACTERIAL FIBRIN-I
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMBERG & SUNSTEIN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                               NAME: Attorney, Strimpel, H
REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: McDonnell, John J
REGISTRATION NUMBER: 26
REFERENCE/DOCKET NUMBER:
                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 125
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 Summer Street
                                                                (617)443-0004
                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reed, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                   (617)443-9292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 30;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                      US/09/211,542A
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                                                                                                                   1874/111
                                                                                                                                                    Harriet M.
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45;
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Query Match
Best Local Similarity
"atches 6; Conserva
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US-09-211-542A-2
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US-07-854-596B-40
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                                                                                                                                                                                                                                                                                                                                       US-07-854-596B-40
                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 312-,1317
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
FONGTH: 747 amino acids
                                                                                                 Sequence 2, Application US/09211542A Patent No. 6210667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PALENTIN Release #10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/854,596B
FILING DATE: 03-UN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hest Local Similarity 100.0%;
Matches 6; Conservative 0
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                                                                 APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMBERG & SUNSTEIN, LLP
                                TITLE OF INVENTION: BACT
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                   143 SVDVEY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 SVDVEY 484
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Ten South Wacker Drive,
                                                                                                                                                                                                                                                                     Conservative
                                                                   Guy L
                                                                                                                                                                                                                                                                                     100.0%;
                                                  BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                     0
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Pred. No. 70;
                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                   DB 1; Length 747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                 COUNTRY: USA
ZII: 0210-2804
COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Attorney, Strimpel, Harriet M. REGISTRATION NUMBER: 37,008
REFERENCE/DOCKET NUMBER: 1874/111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-December-1997
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Strimpel, Har
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 1653
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                              TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                             NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                  APPLICATION NUMBER: US/08/488,940 FILING DATE: 09-JUN-1995 CLASSIFICATION: 514
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
CITY: E
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FILING DATE: 15-December-1998
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                               225 Franklin Street
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Pred. No. 76;
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                                                                                                                                                                                                         Version #1.30
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US-07-854-596B-35
Sequence 35, Application US/07854596B; Patent No. 5434073
GENERAL INFORMATION:
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                                                             RESULT 36
                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-488-940-3
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US-08-488-940-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-488-940-4
                                                                                                                                                                                                      Query Match
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08488940 Patent No. 5854049
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Reed,
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SEQUENCE CHARACTERISTICS:
LENGTH: 800 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 0410-2000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
OPERATION NUMBER: US/08/488,940
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 09-JUN-1995 CLASSIFICATION: 514
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Local Similarity 100.0%;
hes 6; Conservative C
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                                                                                                                                                                                      Local
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                                                                                                         156 SVDVEY 161
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                                                                                                                                        1 SVDVEY 6
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                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                               amino acids
                                                                                                                                                                                                                                                                                 not relevant
                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                    Score 30; DB
Pred. No. 78;
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Pred. No. 77;
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137 SVDVEY 142

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Query Match
Best Local Similarity
When 6; Conserve
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                                                                                                           ; ORGANISM: Hydra vulgaris
US-09-345-473E-25
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US-09-345-473E-25
                                                                                                                                            SOFTWARE: FABISEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 891
TYPE: PRT
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APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558
FILE REFERENCE: 35800/183781
                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/09345473E
Patent No. 6558903
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Best Local Similarity
Matches 6; Conserv
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CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
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INFORMATION FOR SEQ ID NO:
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ATTORINY/AGENT INFORMATION:
NAME: MCDORNELL, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/854,596B
FILLING DATE: 03-UN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dawson, Keith M
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 606
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1 SYDVEY 6
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                                100.0%;
ilarity 100.0%;
Conservative 0
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                                Score 30; DB Pred. No. 87; O; Mismatches
                                                                     DB 4; Length 891;
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                                  Indels
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US-08-488-940-2

Sequence 2, Application Patent No. 5854049
GENERAL INFORMATION:

Application US/08488940

LICANT: Reed, Guy L. LE OF INVENTION: PLA

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TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 amino acids
                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08488940
Patent No. 5854049
GENERAL INFORMATION:
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Best Local :
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ZIP: UZILU-ZUCCOMPOTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,940
FILING DATE: 09-UN-1995
CLASSIFICATION: 514
CLASSIFICATION: 514
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THILE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 225 c
                                                                                                                                               COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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                                                                                                                                                                                                     Boston
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                                                                                                                                                                                                                                                                                                               Reed,
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                                                                                                                                                                                                                                                                         . Guy L.
DN: PLASMIN-RESISTANT STREPTOKINASE
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Pred. No. 1.2e+02;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-488-940-17
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                                         Query Match
Best Local Similarity
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Patent No. 5854049
             Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
TOTAL TOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K.
REGISTARION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/00
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Guy L.
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not
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ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                             CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537 SVDVEY 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
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                                                                                                                                                                                                                                                                                                                                                                                                                                               617/542-8906
                                                                                                                                                                                                                                                                                                          1194 amino acids
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100.0%; Score 30; DB 2; ilarity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismathhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                     not relevant
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Pred. No. 1.2e+02;
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                                                                    Length 1194;
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1 SVDVEY 6

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RESULT 41
US-08-488-940-18
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                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                    Sequence 14, Application US/09470512A Patent No. 6376652
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Best Local (
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ADDLICANT: Reed, Guy
                                                                                              APPLICANT: PhageTech, Inc.
TITLE OF INVENTION: Compositions and methods involving an
TITLE OF INVENTION: gene and its encoded protein
FILE REFERENCE: 21715/1000
CURRENT APPLICATION NUMBER: US/09/470,512A
CURRENT FILING DATE: 1999-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 18:
                                                                                           NUMBER OF SEQ ID NOS: 16
ORGANISM: Bacillus subtilis 9-470-512A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                           TWARE: PatentIn version 3.0 ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617/542-8906
TELEX: 200154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/488,940
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ZIP: 02110-2804
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Pred. No. 1.2e+02;
Pred-retches 0;
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                                                                                                                                                                      essential Staphylococcus
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                                                                                                                                                        RESULT 44
                                                                                                                                         US-09-294-457-3
                                                                                                      Sequence 3, Application US/09294457
Patent No. 6348567
                                                                                            GENERAL
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APPLICANT: Krystal, Gerald
APPLICANT: Rabkin, Simon W.
TITLE OF INVENTION: No. 6348567el Peptides
TITLE OF INVENTION: Ameliorate Cell Death
FILE REFERENCE: 50216/003003
CURRENT APPLICATION NUMBER: US/09/294,457
CURRENT FILING DATE: 1999-04-19

and Their Use to

INFORMATION:

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RESULT 43
US-08-759-599-3
                                                                                                           ; TOPOLOGY: 1i; MOLECULE TYPE: US-08-759-599-3
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Patent No. 591
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Best Local Similarity
                                                     Matches
                                                                  Query Match
Best Local
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TELEX: 3723836
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,599
FILLING DATE: 05-DEC-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-POS/MS-DOS
COBRATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Krystal, Gerald
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
TITLE OF INVENTION: AMELIORATE CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                           TELEPHONE: (200, CONTROL (206) 682-6031
                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                NAME: McMasters, David D.
REGISTRATION NUMBER: 33,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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1 TVDVEY 6
                        1 SYDVEY 6
                                                    Similarity
5; Conserv
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: Washington
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                                                     Conservative
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linear
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66.7%;
                                                                  90.0%;
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Pred. No. 68;
                                                                  Score 27; [
Pred. No. 2.
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 Fifth Avenue
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                                                                                Length 6;
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RESULT 46
US-09-328-352-4507
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US-08-444-646-6
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PRIOR FILING DATE: 1996-12-05
PRIOR APPLICATION NUMBER: US 60/008,233
PRIOR FILING DATE: 1995-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5837
                                                                                                                                   Matches
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DCS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,646
FILING DATE: 19-MAY-1995
CILASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WONG, Wean Khing
REGISTRATION NUMBER: 33.561
REFERENCE/DOCKET NUMBER: 5656-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haake, David A.
APPLICANT: Shang, Ellen S.
TITLE OF INVENTION: Leptospira MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                 Local Similarity es 5; Conserv
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                                                                                                 1 SVDVEY 6
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                                                              TVDVEY 28
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83.3%;
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Pred. No. 2.5e+05;
                                                                                                                                                   Score 27; DB 2;
Pred. No. 1.5e+02;
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                                                                                                                                                                 Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7836, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUWANNI FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7836
LENGTH: 626
LENGTH: 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4507, Application US/09328352

Patent No. 6582958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
APPLICANT: GARY L. BY AND AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4507
LENGTH: 398
                                                                                                                                                                                                                                                               Sequence 5104, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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            COUNTING COUNTING COUNTING COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
TOWNSTTER: PC
TOWNSTTER: PC
TOWNSTER: CUnknown>
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 SVDVDY 235
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COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                   CITY: Waltham
                                                                                                                                                                                    STREET: 100 Beaver Street
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Pred. No. 2.8e+02;
Pred. No. 2.8e+02;
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Pred. No. 1
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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1.7e+02;
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US-08-713-885-3
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application Patent No. 5985833
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/713,885
FILING DATE:
CLASSIFICATION: 514
                                                      ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                       NFORMATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MOSESSON, Michael W.
APPLICANT: Meh, David A.
TITLE OF INVENTION: THROMBIN INHIBITOR
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECHONE: (781)893-5007
TELECHONE: (781)893-8077
TELECHONE: (781)893-8077
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 53202-4497
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...885
SEQUENCE DESCRIPTION: SEQ ID NO: 5104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: YES
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X: (414) 271-3552
N FOR SEQ ID NO: 3:
CHARACTERISTICS:
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                          Wisconsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                              411 East Wisconsin Avenue
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Pred. No. 4.1e+02;
1; Mismatches 0
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Search completed: January 20, 2004, 13:58:13 Job time : 23 secs

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                                                                                                                           ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4271
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US-09-134-001C-4271
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                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4271
LENGTH: 71
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Best Local Similarity
Matches 5; Conserv
                                                            Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4271, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                        APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE; GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                             TYPE: PRT
36
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                               1 SVDVEY 6
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SVDIDY 41
                                                               Conservative
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                                                                            86.7%;
                                                            Score 26; DB 'Pred. No. 42; 2; Mismatches
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Pred. No. 5.9;
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